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Db 601 AACCCCGAGCCACAGAGCTGAAATTTGTAAGCAACTT 638

RESULT 2  
LOCUS 108496 108496 638 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 7 from Patent WO 8701728.  
ACCESSION 108496  
VERSION 108496.1 GI:588788  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 638)  
AUTHORS Fiddes,J.C. and Abraham,J.A.  
TITLE RECOMBINANT FIBROBLAST GROWTH FACTORS  
JOURNAL Patent: WO 8701728-A 7 26-MAR-1987;  
FEATURES  
source Location/Qualifiers  
1. .638  
/organism="unknown"  
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ORIGIN  
Query Match 99.2%; Score 633.2; DB 6; Length 638;  
Best Local Similarity 99.5%; Pred. No. 7.9e-169;  
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAATTCGGGACCGCCACACAGCAGCAGCTGCTGAGCCATGCTGAAGGGGAATCACCA 60  
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Qy 601 AACCCCGAGCCACAGAGCTGAAATTTGTAAGCAACTT 638  
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Qy 181 GGACAGGGACAGAGCGACACAGCAGCAGCTGCTGAGCCATGCTGAAGGGGAATG 240  
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Db 601 AACCCCGAGCCACAGAGCTGAAATTTGTAAGCAACTT 638

RESULT 3  
LOCUS HUMECGPB 638 bp mRNA linear PRI 13-OCT-1995  
DEFINITION Human beta-endothelial cell growth factor (ECGF-beta) mRNA, complete cds.  
ACCESSION M13361  
VERSION M13361.1 GI:181941  
KEYWORDS endothelial cell growth factor-beta; growth factor.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 638)  
AUTHORS Jaye,M., Hawk,R., Burgess,W., Ricca,G.A., Chiu,I.M., Ravera,M.W., O'Brien,S.J., Modi,W.S., Maciag,T. and Drshan,W.N.  
TITLE Human endothelial cell growth factor: cloning, nucleotide sequence, and chromosome localization  
JOURNAL Science 233 (4763), 541-545 (1986)  
MEDLINE 86261805  
PUBMED 3523756  
COMMENT Original source text: Homo sapiens (clone: ECGF[1.29]) brain stem cDNA to mRNA.  
Draft entry and clean copy sequence for [1] kindly provided by M.C.Jaye, 10-OCT-1986.  
The beta-, and alpha-endothelial cell growth factor mRNAs and the aEGF-1 mRNA are probably transcribed from the same gene.

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ORIGIN 1 bp upstream of EcoRI site.  
Query Match 99.2%; Score 633.2; DB 9; Length 638;

Best Local Similarity 99.5%; Pred. No. 7.9e-169; Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTCGGGAACGGCCCAACAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATACCA 60  
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 Db 1 GAATTCGGGAACGGCCCAACAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATACCA 60  
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 Sequencing Center (NISC),  
 QY 301 TATACGCTTCACACACCAATCAGGATGTTTCTTCGGAAGGCTGGAGGAGAAC 360  
 Gaithersburg, Maryland;  
 Db 301 TATACGCTTCACACACCAATCAGGATGTTTCTTCGGAAGGCTGGAGGAGAAC 360  
 Web site: http://www.nisc.nih.gov/  
 QY 361 ATTACACACCTTATATCAAGAGCATGACAGAGAAATGTTGTTGTCCTCAAGA 420  
 Contact: nisc.mgc@nih.gov  
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 QY 421 AGATGGAGCTGCAGACGGGCTCTAACTCACTATGCGCAGAGAAAGCAATCTGTTTC 480  
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 Db 541 GTTTCAGAGGCTCTCTCTGATTAAGAGATCTGTTCTGAGTGTACACACTCCAGAGAA 600  
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 QY 601 AACCCCGAGCCACAGAGCTGATGTTGTAAGCAACTT 638  
 Young, A., Zhang, L.-H. and Green, E.D.  
 Db 601 AACCCCGAGCCACAGAGCTGATGTTGTAAGCAACTT 638

RESULT 4  
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 LOCUS  
 DEFINITION Homo sapiens fibroblast growth factor 1 (acidic), mRNA (cDNA clone  
 MGC:44867 IMAGE:5403677), complete cds.  
 ACCESSION BC032697  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 REFERENCES  
 AUTHORS  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L.,  
 Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S.,  
 Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J.,  
 Abramson R.D., Mullahy J.J., Bosak S.A., McEwan P.J.,  
 McKernan K.O., Malek J.A., Gunaratne P.H., Richards S.,  
 Worley K.C., Hale S., Garcia A.M., Gay L.O., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S.,  
 Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y.,  
 Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D.,  
 Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butlerfield Y.S., Krzywinski M.I., Skalski U., Smalov D.E.,  
 Schnerch A., Schein J.E., Jones S.J. and Marra M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 22388257  
 12477932  
 2 (bases 1 to 1073)  
 Direct Submission  
 Strausberg, R.  
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: http://mgc.nci.nih.gov  
 Contact: MGC help desk  
 Email: c9a9b5-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: http://www.nisc.nih.gov/  
 Contact: nisc.mgc@nih.gov  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,  
 Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W.,  
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Series: IRAX Plate: 69 Row: d Column: 4  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 15055546.  
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 growth factors cause dimerisation of their tyrosine kinase  
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Query Match 94.3%; Score 601.4; DB 9; Length 1073;  
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LOCUS Human mRNA for human heparin-binding growth factor 1/ acidic  
DEFINITION fibroblast growth factor.  
ACCESSION X51943  
VERSION X51943.1 GI:32435  
KEYWORDS fibroblast growth factor; growth factor; heparin-binding growth factor.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2259)  
AUTHORS Chiu, I.M., Wang, W.P. and Lehtoma, K.  
TITLE Alternative splicing generates two forms of mRNA coding for human heparin-binding growth factor 1  
JOURNAL Oncogene 5 (5), 755-762 (1990)  
MEDLINE 90265618  
PUBMED 1693186  
REFERENCE 2 (bases 1 to 2259)  
AUTHORS Chiu, I.M.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-1990) Chiu I.-M., Dept of Internal Medicine, Davis Medical Research Centre, The Ohio State University, 480 West 9th Ave, Columbus OH 43210, USA  
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Query Match 94.3%; Score 601.4; DB 9; Length 2259;  
Best Local Similarity 98.7%; Pred. No. 9.2e-160;  
Matches 627; Conservative 0; Mismatches 6; Indels 2; Gaps 2;  
QY 5 TCGGACCGCCGACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAAATCACCACCTT 64  
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LOCUS 108090  
DEFINITION Sequence 4 from Patent EP 0298723.  
ACCESSION 108090  
VERSION 108090.1 GI:589198  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 638)  
AUTHORS Fiddes, J.C., Abraham, J.A. and Protter, A.



TITLE Recombinant fibroblast growth factors  
JOURNAL Patent: EP 0298723-A1 4 11-JAN-1989;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 86.2%; Score 549.8; DB 6; Length 638;  
Best Local Similarity 98.5%; Pred. No. 4.2e-145;  
Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAAGCGGCCACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCACCACC 62  
DB 55 AGTCTTGAAGCGCCACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCACCACC 114  
QY 63 TTCACAGCCCTGACCGAGAGTTTAACTGCGCTCGAGGAATTCACAGAGCCGCAAACTC 122  
DB 115 TTCACAGCCCTGACCGAGAGTTTAACTGCGCTCGAGGAATTCACAGAGCCGCAAACTC 174  
QY 123 CTCTACTGTAGCAGACGGGGGCCACTTCTCGAGGATCCCTCCGGATGCGCAGCTGGATGGG 182  
DB 175 CTCTACTGTAGCAGACGGGGGCCACTTCTCGAGGATCCCTCCGGATGCGCAGCTGGATGGG 234  
QY 183 ACAGGGACAGAGCGGACGACACATTCAGCTGCGCTGAGTCCGGAAGCCGTGGGGGAG 242  
DB 235 ACAGGGACAGAGCGGACGACACATTCAGCTGCGCTGAGTCCGGAAGCCGTGGGGGAG 294  
QY 243 GTGTATATAAGAGTACCGAGACTGGCCAGTCTTGGCCATGCGCAGCCGCGGCTTTTA 302  
DB 295 GTGTATATAAGAGTACCGAGACTGGCCAGTCTTGGCCATGCGCAGCCGCGGCTTTTA 354  
QY 303 TACGGCTCAGACACCAATAGAGATGTTTCTCGAAGGCTCGAGGAGAACCAT 362  
DB 355 TACGGCTCAGACACCAATAGAGATGTTTCTCGAAGGCTCGAGGAGAACCAT 414  
QY 363 TACACACCTATATATCCAGAGCAGTCGAGAGAAATGTTGTTGGCTTCAAGAAG 422  
DB 415 TACACACCTATATATCCAGAGCAGTCGAGAGAAATGTTGTTGGCTTCAAGAAG 474  
QY 423 AATGGAGCTGCAAAACGGGTCTTAAACTCATATGCGCAGAAAGCAATCTGTTTCTC 482  
DB 475 AATGGAGCTGCAAAACGGGTCTTAAACTCATATGCGCAGAAAGCAATCTGTTTCTC 534  
QY 483 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCT-GGTGTGACCATCCAGAGAAG 541  
DB 535 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCTGGGTGTTGACCATCCAGAGAAG 594  
QY 542 TTTCAGGGGTCTCCTCCTGTTGACCCCAAAATGTTCCCTTGA 586  
DB 595 TTTCAGGGGTCTCCTCCTGTTGACCCCAAAATGTTCCCTTGA 638

RESULT 7  
109138  
LOCUS 109138 638 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 3 from Patent WO 8900198.  
ACCESSION 109138  
VERSION 109138.1 GI:588154  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE UnClassified.  
1 (bases 1 to 638)  
AUTHORS Fiddes,J.C., Abraham,J.A. and Protter,A.  
JOURNAL Patent: WO 8900198-A 3 12-JAN-1989;  
FEATURES Location/Qualifiers  
source 1..638  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 86.2%; Score 549.8; DB 6; Length 638;  
Best Local Similarity 98.5%; Pred. No. 4.2e-145;  
Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAAGCGGCCACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCACCACC 62  
DB 55 AGTCTTGAAGCGCCACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCACCACC 114

QY 63 TTCACAGCCCTGACCGAGAGTTTAACTGCGCTCGAGGAATTCACAGAGCCGCAAACTC 122  
DB 115 TTCACAGCCCTGACCGAGAGTTTAACTGCGCTCGAGGAATTCACAGAGCCGCAAACTC 174  
QY 123 CTCTACTGTAGCAGACGGGGGCCACTTCTCGAGGATCCCTCCGGATGCGCAGCTGGATGGG 182  
DB 175 CTCTACTGTAGCAGACGGGGGCCACTTCTCGAGGATCCCTCCGGATGCGCAGCTGGATGGG 234  
QY 183 ACAGGGACAGAGCGGACGACACATTCAGCTGCGCTGAGTCCGGAAGCCGTGGGGGAG 242  
DB 235 ACAGGGACAGAGCGGACGACACATTCAGCTGCGCTGAGTCCGGAAGCCGTGGGGGAG 294  
QY 243 GTGTATATAAGAGTACCGAGACTGGCCAGTCTTGGCCATGCGCAGCCGCGGCTTTTA 302  
DB 295 GTGTATATAAGAGTACCGAGACTGGCCAGTCTTGGCCATGCGCAGCCGCGGCTTTTA 354  
QY 303 TACGGCTCAGACACCAATAGAGATGTTTCTCGAAGGCTCGAGGAGAACCAT 362  
DB 355 TACGGCTCAGACACCAATAGAGATGTTTCTCGAAGGCTCGAGGAGAACCAT 414  
QY 363 TACACACCTATATATCCAGAGCAGTCGAGAGAAATGTTGTTGGCTTCAAGAAG 422  
DB 415 TACACACCTATATATCCAGAGCAGTCGAGAGAAATGTTGTTGGCTTCAAGAAG 474  
QY 423 AATGGAGCTGCAAAACGGGTCTTAAACTCATATGCGCAGAAAGCAATCTGTTTCTC 482  
DB 475 AATGGAGCTGCAAAACGGGTCTTAAACTCATATGCGCAGAAAGCAATCTGTTTCTC 534  
QY 483 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCT-GGTGTGACCATCCAGAGAAG 541  
DB 535 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCTGGGTGTTGACCATCCAGAGAAG 594  
QY 542 TTTCAGGGGTCTCCTCCTGTTGACCCCAAAATGTTCCCTTGA 586  
DB 595 TTTCAGGGGTCTCCTCCTGTTGACCCCAAAATGTTCCCTTGA 638

RESULT 8

BTFGPAR  
LOCUS BTFGPAR 4005 bp mRNA linear MAM 18-NOV-1993  
DEFINITION Bovine mRNA for acidic fibroblast growth factor.  
ACCESSION X13221 S47526  
VERSION X13221.1 GI:347  
KEYWORDS fibroblast growth factor acidic; growth factor.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 4005)  
AUTHORS Halley,C., Courtois,Y. and Laurent,M.  
TITLE Nucleotide sequence of bovine acidic fibroblast growth factor cDNA  
JOURNAL Nucleic Acids Res. 16 (22), 10913 (1988)  
MEDLINE 89083506  
PUBMED 3205724  
REFERENCE 2

Philippe,J.M., Renaud,F., Desset,S., Laurent,M., Mallet,J.,  
Courtois,Y. and Edwards,J.B.  
Cloning of two different 5' untranslated exons of bovine acidic  
fibroblast growth factor by the single strand ligation to  
single-stranded cDNA methodology  
Biochem. Biophys. Res. Commun. 188 (2), 843-850 (1992)

JOURNAL 93075172  
MEDLINE 1280126  
PUBMED 3 (bases 1 to 4005)  
REFERENCE 3 (bases 1 to 4005)  
AUTHORS Halley,C.  
TITLE Direct Submission

Submitted (12-OCT-1988) Halley C., Inserm U118, 29 Rue Wilhem  
75016 Paris, France  
COMMENT see M13439 for overlapping sequence.  
FEATURES Location/Qualifiers  
1..4005  
/organism="Bos taurus"  
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918..11385

CDS

/note="unnamed protein product; acidic fibroblast growth factor (AA 1 - 155)"  
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/db\_xref="SWISS-PROT:P03968"  
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ORIGIN

Query Match 77.1%; Score 491.8; DB 4; Length 4005;  
Best Local Similarity 88.3%; Pred. No. 1.4e-128;  
Matches 557; Conservative 0; Mismatches 72; Indels 2; Gaps 2;

QY 9 GAACGGCCACAGAGGAGCTGTGAGCCATGCTGAGAGGAGAAATACACCACTTCA 68  
DB 888 GAAACGACCAACACAGAGGAGCTGTGAGCCATGCTGAGAGGAGAAATACACCACTTCA 947  
QY 69 GCCCTGACGAGAGAGTTAATCTGCTCCAGGCAATACAAAGAGCCCAAACTCTCTAC 128  
DB 948 GCCCTGACTGAGAGTTAATCTGCTCCAGGCAATACAAAGAGCCCAAACTCTCTAC 1007  
QY 129 TGTAGCAAGGGGGGCACTTCTGAGATCTTCTGAGTGGCAGACAGTGGATGGAGCAAG 188  
DB 1008 TGCAGCAAGGGGGGCACTTCTGAGATCTTCTGAGTGGCAGACAGTGGATGGAGCAAG 1067  
QY 189 GACAGAGGAGCAGCAGCATTCAGCTGCAGCTCAGTGGGAAAGCGTGGGGAGGTGTAT 248  
DB 1068 GACAGAGGAGCAGCAGCATTCAGCTGCAGCTCAGTGGGAAAGCGTGGGGAGGTGTAT 1127  
QY 249 ATAAAGATACCGAGAGCTGGCAGTCTTGGGCATGAGACAGCGGGCTTTTATACGC 308  
DB 1128 ATAAAGATACCGAGAGCTGGCAGTCTTGGGCATGAGACAGCGGGCTTTTATACGC 1187  
QY 309 TCACAGACACAAATAGGAATGTTTCTGAAAGGCTGAGAGAGCAACATTACAAC 368  
DB 1188 TCACAGACACAAATAGGAATGTTTCTGAAAGGCTGAGAGAGCAACATTACAAC 1247  
QY 369 ACCTATATATCAAGAGCATGAGAGAGATGTTGTTGGCTTCAAGAGAGAAATGGG 428  
DB 1248 ACCTATATATCAAGAGCATGAGAGAGATGTTGTTGGCTTCAAGAGAGAAATGGG 1307  
QY 429 AGCTGCAAGCGGCTCTAAATCTGAGCAAGAAATCTGTTCTTCCCTG 488  
DB 1308 AGCTGCAAGCGGCTCTAAATCTGAGCAAGAAATCTGTTCTTCCCTG 1367  
QY 489 CAGTCTCTCTGATTAAGAGATCTGTTCTGTTGTTGACACTCCAGAGAGTTTGA 547  
DB 1368 CAGTCTCTCTGATTAAGAGATCTGTTGTTGTTGACACTCCAGAGAGTTTGA 1427  
QY 548 GGGGTCTCACTGCTGACCCCAAAATGTTCCCTGACCATTTGGCTGAGCTTAACCC 607  
DB 1428 GGGGTCTCACTGCTGACCCCAAAATGTTCCCTGACCATTTGGCTGAGCTTAACCC 1486  
QY 608 AGCCACAGAGCTCTGAATTTGTAAGCACTT 638  
DB 1487 GGGCCACAGAGCTCTGAATTTGTAAGCACTT 1517

RESULT 9  
AR380845  
LOCUS AR380845 430 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1390 from patent US 6607879.  
ACCESSION AR380845  
VERSION AR380845.1 GI:40088479  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 490)  
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.  
TITLE Compositions for the detection of blood cell and immunological response gene expression  
JOURNAL Patent: US 6607879-A 1390 19-AUG-2003;  
FEATURES Location/Qualifiers  
source 1..490  
/organism="unknown"

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Query Match 76.1%; Score 485.2; DB 6; Length 490;  
Best Local Similarity 99.4%; Pred. No. 9.7e-127;  
Matches 487; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 29 CTGCTGAGCCTGCTGAGAGGAGAAATCACCACCTTTCACAGCCCTGACGAGAGTTTAA 88  
DB 1 CTGCTGAGCCTGCTGAGAGGAGAAATCACCACCTTTCACAGCCCTGACGAGAGTTTAA 60  
QY 89 TCTGCTCCAGGAGAAATCAAGAGCCCAAACTCTCTTCTTCTGAGCAACGGGGGCACTT 148  
DB 61 TCTGCTCCAGGAGAAATCAAGAGCCCAAACTCTCTTCTTCTGAGCAACGGGGGCACTT 120  
QY 149 CTGAGAGATCTCTCCGATGCGACAGTGGATGGGACAGGAGGACAGGAGCCAGCAGCAT 208  
DB 121 CTGAGAGATCTCTCCGATGCGACAGTGGATGGGACAGGAGGACAGGAGCCAGCAGCAT 180  
QY 209 TCAGCTGAGCTCAGTGGGAGAGCGTGGGAGAGGTGTATATAAGAGTACCAGAGCTGG 268  
DB 181 TCAGCTGAGCTCAGTGGGAGAGCGTGGGAGAGGTGTATATAAGAGTACCAGAGCTGG 240  
QY 269 CCAGTACTTGGCCTGACACGAGCGGCTTTTATAGGCTCACAGACACCAATGAGGA 328  
DB 241 CCAGTACTTGGCCTGACACGAGCGGCTTTTATAGGCTCACAGACACCAATGAGGA 300  
QY 329 ATGTTTGTCTGAAAGGCTGGAGGAGAACATTACAACCTATATATCAAGAGCA 388  
DB 301 ATGTTTGTCTGAAAGGCTGGAGGAGAACATTACAACCTATATATCAAGAGCA 360  
QY 389 TSCAGAGAAATTTGTTTGGCTTCAAGAGAGAAATGGGAGCTGCAAGCGGCTCTAA 448  
DB 361 TSCAGAGAAATTTGTTTGGCTTCAAGAGAGAAATGGGAGCTGCAAGCGGCTCTCG 420  
QY 449 AACTCCTATGCGCAGAGAAATCTGTTTCTTCCCTGCGAGTCTTCTTCTGATTAAG 508  
DB 421 GACTCCTATGCGCAGAGAAATCTGTTTCTTCCCTGCGAGTCTTCTTCTGATTAAG 480  
QY 509 AGATCTGTC 518  
DB 481 AGATCTGTC 490

RESULT 10  
HSAFGF  
LOCUS HSAFGF 490 bp mRNA linear PRI 02-AUG-1993  
DEFINITION H sapiens aFGF mRNA for acidic fibroblast growth factor.  
ACCESSION X65778  
VERSION X65778.1 GI:396163  
KEYWORDS fibroblast growth factor; fibroblast growth factor acidic.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 490)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Yu,Y.L., Kha,H., Golden,J.A., Migchielsen,A.A., Goetzl,E.J. and Turk,C.W.  
TITLE An acidic fibroblast growth factor protein generated by alternate splicing acts like an antagonist  
JOURNAL J. Exp. Med. 175 (4), 1073-1080 (1992)  
MEDLINE 92202857  
PUBMED 1372643

FEATURES  
source 1..490  
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ORIGIN

Query Match 76.1%; Score 485.2; DB 9; Length 490;  
 Best Local Similarity 99.4%; Pred. No. 9.7e-127;  
 Matches 487; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 29 CTGCTGAGCCATGCTGAGGGGAAATCAACACCTTCAAGCCCTGACCGAGAGTTTAA 88  
 DB 1 CTGCTGAGCCATGCTGAGGGGAAATCAACACCTTCAAGCCCTGACCGAGAGTTTAA 60

QY 89 TCTGCTCCAGGGAATTAACAAGGCCAAACTCTCTACTGTTAGCAAGGGGGCACTT 148  
 DB 61 TCTGCTCCAGGGAATTAACAAGGCCAAACTCTCTACTGTTAGCAAGGGGGCACTT 120

QY 149 CTTGAGGATCTCTCCGATGGCAGAGTGGATGGGACAAGGACAGGACGACACAT 208  
 DB 121 CTTGAGGATCTCTCCGATGGCAGAGTGGATGGGACAAGGACGACGACAT 180

QY 209 TCAGCTCGAGCTAGTCCGGAAGCGTGGGGAGGTGTATATTAAGAGTACGAGACTGG 268  
 DB 181 TCAGCTCGAGCTAGTCCGGAAGCGTGGGGAGGTGTATATTAAGAGTACGAGACTGG 240

QY 269 CCAGTACTTGGCCATGACACACCGAGCGGCTTTTATACGGCTCAGACACCAATGAGGA 328  
 DB 241 CCAGTACTTGGCCATGACACACCGAGCGGCTTTTATACGGCTCAGACACCAATGAGGA 300

QY 329 ATGTTTCTTGGGAAGGCTGGAGGAGAACATTAACACCTTATATATCAAGAGCA 388  
 DB 301 ATGTTTCTTGGGAAGGCTGGAGGAGAACATTAACACCTTATATATCAAGAGCA 360

QY 389 TCAGAGAGGAATGTTTGTGGCTCAAGAGAAATGGAGCTGCAACCGGCTCTTAA 448  
 DB 361 TCAGAGAGGAATGTTTGTGGCTCAAGAGAAATGGAGCTGCAACCGGCTCTTAA 420

QY 449 AACTCATTATGCGCAAGAGCAATCTGTTCTCCCGCTGCGACGTCTCTTCTGATTAAG 508  
 DB 421 GACTCATTATGCGCAAGAGCAATCTGTTCTCCCGCTGCGACGTCTCTTCTGATTAAG 480

QY 509 AGATCTGTC 518  
 DB 481 AGRCTGTC 490

RESULT 11  
 BOVFGFAA  
 LOCUS Bovine acidic eye-derived fibroblast growth factor (EDGF II) mRNA, complete cds.  
 M35608  
 VERSION M35608.1 GI:163047  
 KEYWORDS acidic eye-derived fibroblast growth factor.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 668)  
 AUTHORS Alterio, J., Halley, C., Brou, C., Soussi, T., Courtois, Y. and Laurent, M.  
 TITLE Characterization of a bovine acidic PGF cDNA clone and its expression in brain and retina  
 JOURNAL FEBS Lett. 242 (1), 41-46 (1988)  
 MEDLINE 89078619  
 PUBMED 2849564  
 COMMENT Original source text: Bovine retina, cDNA to mRNA.  
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 source Location/Qualifiers  
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 /organism="Bos taurus"  
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 91..558  
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ORIGIN

Query Match 74.3%; Score 474.2; DB 4; Length 668;  
 Best Local Similarity 88.3%; Pred. No. 1.3e-123;  
 Matches 538; Conservative 0; Mismatches 68; Indels 3; Gaps 2;

QY 9 GAAGCCGCCAACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCAACACCTTCA 68  
 DB 61 GAAGCCGCCAACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCAACACCTTCA 120

QY 69 GCCCTGACCGAGAGCTTTAATCTGCTCCAGGGAATTAACAAGGCCAACTCTCTAC 128  
 DB 121 GCCCTGACCGAGAGCTTTAATCTGCTCCAGGGAATTAACAAGGCCAACTCTCTAC 180

QY 129 TGTAGCAACCGGGGCGCACTTCTCTGAGGATCTTCCGATGGCAGAGTGGATGGGACAAG 188  
 DB 181 TGTAGCAACCGGGGCGCACTTCTCTGAGGATCTTCCGATGGCAGAGTGGGACGAAG 240

QY 189 GACGAGGCGACCGACACATTCAGCTCGAGCTCAGTSCGGAAGCGTGGGGAGGTGTAT 248  
 DB 241 GACGAGGCGACCGACACATTCAGCTCGAGCTCAGTSCGGAAGCGTGGGGAGGTGTAT 300

QY 249 ATAAGAGTAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGGCTTTTATACGGC 308  
 DB 301 ATAAGAGTAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGGCTTTTATACGGC 360

QY 309 TCACGACACCAATGAGGAATGTTTGTCTCGGAAGGCTGSGAGGACCACTTACAC 368  
 DB 361 TCACGACACCAATGAGGAATGTTTGTCTCGGAAGGCTGSGAGGACCACTTACAC 420

QY 369 ACTATATATCCAGAAGCAATCCAGAGAAATTTGTTTGTGGCTCAAGAAGATGGG 428  
 DB 421 ACTATATATCCAGAAGCAATCCAGAGAAATTTGTTTGTGGCTCAAGAAGATGGG 480

QY 429 AGCTCGAAGCGGCTTAAACATCTATGCGCAAGCAATCTGTTCTCCCGCTG 488  
 DB 481 AGCTCGAAGCGGCTTAAACATCTATGCGCAAGCAATCTGTTCTCCCGCTG 540

QY 489 CAGTCTCTTCTGATTAAGAGATCTGTTCTGCG--TGTGACCACTCCAGAGAGTTTTCG 546  
 DB 541 CAGTCTCTTCTGATTAAGAGATCTGTTCTGCGTGTGAGCCACTCCAGAGAGATCTGA 600

QY 547 AGGGGTCTCTACCTGTTGACCCCAAAATGTTCCCTTGACCAATGCGTCCGCTTAAGCCC 606  
 DB 601 AGGGGTCTCTACCTGTTGACCCCAAAATGTTCCCTTGACCAATGCGTCCGCTTAAGCCC 659

QY 607 CAGCCGCCA 615  
 DB 660 TGGCCGCCA 668

RESULT 12  
 BTEDGF  
 LOCUS Bovine mRNA for EDGF II (acidic eye-derived growth factor II).  
 DEFINITION Bovine mRNA for EDGF II (acidic eye-derived growth factor II).  
 ACCESSION X14032 S47526  
 VERSION X14032.1 GI:322  
 KEYWORDS acidic eye-derived growth factor II; growth factor.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 668)  
 AUTHORS Alterio, J., Halley, C., Brou, C., Soussi, T., Courtois, Y. and Laurent, M.  
 TITLE Characterization of a bovine acidic PGF cDNA clone and its expression in brain and retina  
 JOURNAL FEBS Lett. 242 (1), 41-46 (1988)  
 MEDLINE 89078619  
 PUBMED 2849564  
 REFERENCE 2  
 AUTHORS Philippe, J.M., Renaud, F., Desset, S., Laurent, M., Mallet, J., Courtois, Y. and Edwards, J.B.  
 TITLE Cloning of two different 5' untranslated exons of bovine acidic fibroblast growth factor by the single strand ligation to single-stranded cDNA methodology  
 JOURNAL Biochem. Biophys. Res. Commun. 188 (2), 843-850 (1992)  
 MEDLINE 93075172  
 PUBMED 1280126  
 FEATURES Location/Qualifiers

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CDS

ORIGIN

Query Match 74.3%; Score 474.2; DB 4; Length 668;  
Best Local Similarity 88.3%; Pred. No. 1.3e-123;  
Matches 538; Conservative 0; Mismatches 68; Indels 3; Gaps 2;

QY 9 GAACGGCCACACAGCAGCTGCTGAGCCATGCGTGAAGGGGAATCATCCTTCACA 68  
DB 61 GAACAGCCACACACAGCAGCTGCTGAGCCATGCGTGAAGGGGAATCATCCTTCAG 120  
QY 69 GCCCTGACCGAGAGTTTAACTCTCTCCAGGGAATTTACAGAGGCCCAAACTCTCTAC 128  
DB 121 GCCCTGACCTGAGAGTTTAACTCTCTCTGAGCAATTTACAGAGGCCCAAACTCTCTAC 180  
QY 129 TGTAGCAAGCGGGGCCACTTCTCTGAGGATCTTCCGATGGGACAGTGTGAGGACAG 188  
DB 181 TGCAGCAAGCGGGGGCTACTTCTGAGAACTCTCTCCAGATGGCAGTGTGAGGACAG 240  
QY 189 GACAGAGCGCAGCAGACATTCAGCTGACGTCTGCTGCGAAAGCGTGGGCGAGTGTAT 248  
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QY 249 ATAAAGAGTACCGAGCTGGCCAGTCTTGGCCATGGACACCGAGCGGCTTTTATAGGG 308  
DB 301 ATTAAGAGTACCGAGCTGGCCAGTCTTGGCCATGGACACCGAGCGGCTTTTATAGGG 360  
QY 309 TCACAGACACCAATAGGAGATTTGCTGCTGGAAGGCTGGAGGAGACCATTTACAC 368  
DB 361 TCACAGACACCAATAGGAGATTTGCTGCTGGAAGGCTGGAGGAGACCATTTACAC 420  
QY 369 ACCTATATCAAGAAGCATCAGAGAAATGTGTTGTTGGCTCTCAGAGAAATGGG 428  
DB 421 ACCTATATCAAGAAGCATCAGAGAAATGTGTTGTTGGCTCTCAGAGAAATGGG 480  
QY 429 AGCTGCAAGCGGCTCTAAACTCACTATGCGCAGAAAGCAATCTTGTCTCCCGCTG 488  
DB 481 AGCTGCAAGCGGCTCTAAACTCACTATGCGCAGAAAGCAATCTTGTCTCCCGCTG 540  
QY 489 CCAGTCTCTTGTGATTAAGAGATCTTGTCTG--TGTGACCACTCCAGAGAGTTTG 546  
DB 541 CCAGTCTCTTGTGATTAAGAGATCTTGTCTG--TGTGACCACTCCAGAGAGTTTG 600  
QY 547 AGGGTCTCTACCTGTTGTGACCCCAAAATGTTCTGACCATTTGCTGCGCTAACCCC 606  
DB 601 AGGGTCTCTACCTGTTGTGACCCCAAAATGTTCTGACCATTTGCTGCGCTAACCCC 659  
QY 607 CAGCCCA 615  
DB 660 TGGCCCA 668

RESULT 13  
A49428  
LOCUS A49428 8501 bp DNA circular PAT 07-MAR-1997  
DEFINITION Sequence 1 from Patent WO9608572.  
ACCESSION A49428  
VERSION A49428.1 GI:2302907  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 8501)  
Cameron,B. and Crouzet,J.  
METHOD FOR THE PRODUCTION OF RECOMBINANT PROTEINS, PLASMIDS AND MODIFIED CELLS  
JOURNAL Patent: WO 9608572-A 1 21-MAR-1996;  
COMMENT RHONE-POULENC RORER SA (FR)  
Other publication AU 3475495 960329  
Other publication FR 2724665 960322.  
FEATURES  
Location/Qualifiers  
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/db\_xref="taxon:32644"

ORIGIN

Query Match 73.8%; Score 470.6; DB 6; Length 8501;  
Best Local Similarity 99.2%; Pred. No. 1.5e-122;  
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 39 ATGCGTGAAGGGGAATACCACTTCCAGCCCTGACCGAGAAGTTTAACTCTGCTCCA 98  
DB 108 ATGCGTGAAGGGGAATACCACTTCCAGCCCTGACCGAGAAGTTTAACTCTGCTCCA 167  
QY 99 GCGAATTACAGAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCTGAGGATC 158  
DB 168 GCGAATTACAGAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCTGAGGATC 227  
QY 159 CTTCCGATGGCAGACGTGATGGGACAGGAGGAGGACACAGACATTCAGCTGCAG 218  
DB 228 CTTCCGATGGCAGACGTGATGGGACAGGAGGAGGACACAGACATTCAGCTGCAG 287  
QY 219 CTCAGTCCGGAAGCGTGGGGAGGCTGTATATAAGAGTACCGAGCTGCCAGTACTTG 278  
DB 288 CTCAGTCCGGAAGCGTGGGGAGGCTGTATATAAGAGTACCGAGCTGCCAGTACTTG 347  
QY 279 GCATGGACACCGCGGGCTTTTATAGCGCTCAGACACACCAATATGAGGATTTGTTTC 338  
DB 348 GCATGGACACCGCGGGCTTTTATAGCGCTCAGACACACCAATATGAGGATTTGTTTC 407  
QY 339 CTGGAAGAGCTCGAGAGCAACCATTAACAACCTATATATCCAGAGCATCGAGAGAG 398  
DB 408 CTGGAAGAGCTCGAGAGCAACCATTAACAACCTATATATCCAGAGCATCGAGAGAG 467  
QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACGCGGCTCAAACTCACTAT 458  
DB 468 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACGCGGCTCAAACTCACTAT 527  
QY 459 GCGCAGAGCAACTGTTGTTCTCCCTCCAGCTCTCTCTGATTAAAGAGATCTG 515  
DB 528 GCGCAGAGCAACTGTTGTTCTCCCTCCAGCTCTCTCTGATTAAAGAGATCTG 584

RESULT 14  
108499  
LOCUS 108499 481 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 13 from Patent WO 8701728.  
ACCESSION 108499  
VERSION 108499.1 GI:588791  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 481)  
AUTHORS Fiddes,J.C. and Abraham,J.A.  
TITLE RECOMBINANT FIBROBLAST GROWTH FACTORS  
JOURNAL Patent: WO 8701728-A 13 26-MAR-1987;  
FEATURES Location/Qualifiers  
source 1..481  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 72.7%; Score 464; DB 6; Length 481;  
Best Local Similarity 98.9%; Pred. No. 1e-120;  
Matches 467; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 37 CCATGGCTGAAGGGGAATCAACCATCTTCACGCCCTTCACCGAGAAGTTTAACTCTGCTC 96  
DB 1 CCATGGCTGAAGGGGAATCAACCATCTTCACGCCCTTCACCGAGAAGTTTAACTCTGCTC 60

QY 97 CAGGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCGAGA 156  
DB 61 CAGGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCGAGA 120  
QY 157 TCCTTCGGATGCGCAGTGGATCGGACCAAGGACAGGACGACGACATTCAGCTGC 216  
DB 121 TCCTTCGGATGCGCAGTGGATCGGACCAAGGACAGGACGACGACATTCAGCTGC 180  
QY 217 AGCTCAGTCCGGAAGCGTGGGAGGCTGTATATAAGAGTACCGAGACTGGCCAGTCT 276  
DB 181 AGCTCAGTCCGGAAGCGTGGGAGGCTGTATATAAGAGTACCGAGACTGGCCAGTCT 240  
QY 277 TGGCCATGACACCGACGGGCTTTTATAGGCTCACAGACCAAAATGAGGAATGTTGT 336  
DB 241 TGGCTATGACACCGACGGGCTTTTATAGGCTCACAGACCAAAATGAGGAATGTTGT 300  
QY 337 TCCTGGAAGGCTGGAGGAAACATTTACACACTATATATCCAGAGCATGACAGAG 396  
DB 301 TCCTGGAAGGCTGGAGGAAACATTTACACACTATATATCCAGAGCATGACAGAG 360  
QY 397 AGAATTGGTTTGTGGCTTCAAGGAAGTGGAGCTGCAAGCGGCTCTTAAACTCACT 456  
DB 361 AGAATTGGTTTGTGGCTTCAAGGAAGTGGAGCTGCAAGCGGCTCTTAAACTCACT 420  
QY 457 ATGGCCAGAAAGCAATCTTGTCTTCCCTGCGAGTCTCTCTGTATTAAG 508  
DB 421 ATGGCCAGAAAGCAATCTTGTCTTCCCTGCGAGTCTCTCTGTATTAAG 472

RESULT 15  
LOCUS 109297 481 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 10 from Patent WO 890471.  
ACCESSION 109297  
VERSION 109297.1 GI:588003  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 481)  
AUTHORS Talmadge,K.D. and Hilliker,S.  
TITLE RECOMBINANT DNA CONSTRUCTS CONTAINING AN R3 PROMOTER  
JOURNAL Patent: WO 890471-A 10 23-MAR-1989;  
FEATURES  
source 1. 481  
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/mol\_type="unassigned DNA"

ORIGIN  
Query Match 72.7%; Score 464; DB 6; Length 481;  
Best Local Similarity 98.9%; Pred. No. 1e-120;  
Matches 467; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 37 CCATGGCTGAAGGGGAATCACCACCTTACAGCCCTGACCGAGAGTTTAACTGCTC 96  
DB 1 CCATGGCTGAAGGGGAATCACCACCTTACAGCCCTGACCGAGAGTTTAACTGCTC 60

QY 97 CAGGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCGAGA 156  
DB 61 CAGGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCGAGA 120

QY 157 TCCTTCGGATGCGCAGTGGATCGGACCAAGGACAGGACGACGACATTCAGCTGC 216  
DB 121 TCCTTCGGATGCGCAGTGGATCGGACCAAGGACAGGACGACGACATTCAGCTGC 180

QY 217 AGCTCAGTCCGGAAGCGTGGGAGGCTGTATATAAGAGTACCGAGACTGGCCAGTCT 276  
DB 181 AGCTCAGTCCGGAAGCGTGGGAGGCTGTATATAAGAGTACCGAGACTGGCCAGTCT 240

QY 277 TGGCCATGACACCGACGGGCTTTTATAGGCTCACAGACCAAAATGAGGAATGTTGT 336  
DB 241 TGGCTATGACACCGACGGGCTTTTATAGGCTCACAGACCAAAATGAGGAATGTTGT 300

QY 337 TCCTGGAAGGCTGGAGGAAACATTTACACACTATATATCCAGAGCATGACAGAG 396  
DB 301 TCCTGGAAGGCTGGAGGAAACATTTACACACTATATATCCAGAGCATGACAGAG 360

QY 397 AGAATTGGTTTGTGGCTTCAAGGAAGTGGAGCTGCAAGCGGCTCTTAAACTCACT 456

DB 361 AGAATTGGTTTGTGGCTTCAAGGAAGTGGAGCTGCAAGCGGCTCTTAAACTCACT 420  
QY 457 ATGGCCAGAAAGCAATCTTGTCTTCCCTGCGAGTCTCTCTGTATTAAG 508  
DB 421 ATGGCCAGAAAGCAATCTTGTCTTCCCTGCGAGTCTCTCTGTATTAAG 472

Search completed: August 24, 2004, 20:02:46  
Job time : 4177 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 16:28:39 ; Search time 441 Seconds  
(without alignments)  
6145.919 Million cell updates/sec

Title: US-10-022-554A-3  
Perfect score: 638  
Sequence: 1 gaattcgggaacgcgcaca.....cctgaatttgaagcaactt 638

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002s.\*  
7: Geneseq2003as.\*  
8: Geneseq2003bs.\*  
9: Geneseq2003cs.\*  
10: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	638	100.0	638	8	ACF04029 Thrombin
2	633.2	99.2	638	1	AAN70788 Complete
3	633.2	99.2	638	2	AAT37503 Human bet
4	633.2	99.2	638	2	AAN74350 Human end
5	633.2	99.2	638	2	AAX01723 Human end
6	633.2	99.2	638	8	ACF04028 Thrombin
7	622.2	97.5	639	2	AAT45985 Human end
8	601.8	94.3	2357	9	ACC42968 Human FIB
9	601.8	94.3	4087	7	ABX63225 Human cDN
10	549.8	86.2	638	1	AAN93088 Acidic fi
11	470.6	73.8	8501	2	AAT12907 Novel exp
12	464	72.7	481	1	AAN71029 Sequence
13	464	72.7	481	1	AAN90994 Partially
14	463.2	72.6	468	6	ABV78179 Human DNA
15	463.2	72.6	468	6	ABZ35755 Human pol
16	463.2	72.6	468	6	ABX09998 Human DNA
17	463.2	72.6	468	6	AAK98918 Human aci
18	463.2	72.6	468	6	ABL91720 Human pol
19	460	72.1	496	2	AAQ03871 Synthetic

## ALIGNMENTS

RESULT 2	
AAAN70788	
ID	AAAN70788 standard; cDNA; 638 BP.
XX	
XX	AAAN70788;
XX	
XX	25-MAR-2003 (revised)
DT	13-MAY-1991 (first entry)
DE	
DE	Complete cDNA sequence of human endothelial cell growth factor (ECGF).
KW	Endothelial cell regeneration; blood vessel regeneration; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	CDS 39..506

FT mat\_peptide /tag= a 42. .83 421 AGAATGGAGCTGCAACGGCGTCTCGACTCTACTATGCGCAGAGAAAGCAATCTGTTTC 480  
 FT /tag= b 481 TCCCTCGCGAGTCTCTCTGATTAAGAGATCTGTTCTGTTGACCACTCCAGAGAA 540  
 FT /product= "Beta ECGF" 481 TCCCTCGCGAGTCTCTCTGATTAAGAGATCTGTTCTGTTGACCACTCCAGAGAA 540  
 FT /tag= c 541 GTTTCGAGGGTCTCTACCTGCTGACCCCAAAATGTTCCCTTGACCACTTGCTGCGCT 600  
 FT /product= "Acidic FGF" 541 GTTTCGAGGGTCTCTACCTGCTGACCCCAAAATGTTCCCTTGACCACTTGCTGCGCT 600  
 FT /tag= d 601 AACCCCGCCGACAGAGCTGAAATTTGTAAGCACTT 638  
 FT /product= "Alpha ECGF" 601 AACCCCGCCGACAGAGCTGAAATTTGTAAGCACTT 638  
 XX W08705332-A.  
 XX 11-SEP-1987.  
 XX 02-MAR-1987; 87WO-US000425.  
 XX 03-MAR-1986; 86US-00835594.  
 XX (MELO-) MELOY LAB INC.  
 XX (RORE ) RORER BIOTECHNOLOGY INC.  
 XX Jaye M, Burgess W, Maciag T, Drohan W;  
 XX WPI; 1987-264128/37.  
 XX P-PSDB; AAP70482.  
 XX Human endothelial cell growth factor - produced by recombinant DNA techniques, useful for wound healing.  
 XX Example; Fig 8; 43pp; English.  
 XX To screen the human brain stem cDNA library for clones contg. ECGF inserts, a specific oligonucleotide was designed. This oligonucleotide was based upon a partial AA sequence analysis of the amino terminus of ECGF (see AAP70480 and AAP70481). Fig 3c sets forth for comparison the AA sequence of cyanogen bromide-cleaved bovine alpha and beta ECGF (AAP70834). The two clones that were isolated, ECGF clones 1 and 29, were analysed in further detail. The nucleotide sequence of these clones and the AA sequence deduced from the nucleic acid sequence is shown in Fig 8 (see AAP70788 and AAP70482). (Updated on 25-MAR-2003 to correct PA field.)  
 XX Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
 SQ

Query Match 99.2%; Score 633.2; DB 1; Length 638;  
 Best Local Similarity 99.5%; Pred. No. 3.5e-186;  
 Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAATTCGGAGCGGCCACACGACGAGCTGCTGAGCCATGCTGGAAGGGGAATCACCA 60  
 DB 1 GAATTCGGAGCGGCCACACGACGAGCTGCTGAGCCATGCTGGAAGGGGAATCACCA 60  
 QY 61 CCTTCACAGCCCTGACCGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAC 120  
 DB 61 CCTTCACAGCCCTGACCGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAC 120  
 QY 121 TCCCTACTGTATAGACGCGGGGCCACTTCTCGAGATCTTCCGATGGCAGTGGATG 180  
 DB 121 TCCCTACTGTATAGACGCGGGGCCACTTCTCGAGATCTTCCGATGGCAGTGGATG 180  
 QY 181 GGACAGGGACGAGGACGACGACGACATTCAGCTGCGAGTCTGCGGAAAGCGTGGGG 240  
 DB 181 GGACAGGGACGAGGACGACGACGACATTCAGCTGCGAGTCTGCGGAAAGCGTGGGG 240  
 QY 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTCTTGGCCATGACACCGAGGGCTTT 300  
 DB 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTCTTGGCCATGACACCGAGGGCTTT 300  
 QY 301 TATAGGCTCACACACCAATAGGAATGTTGTTCTTGAAGAGCTGGAGAGAAC 360  
 DB 301 TATAGGCTCACACACCAATAGGAATGTTGTTCTTGAAGAGCTGGAGAGAAC 360  
 QY 361 ATTACACCTTATATCCAGAGCATGCGAGAGAAATGGTTGTTGCGCTCAAGA 420  
 DB 361 ATTACACCTTATATCCAGAGCATGCGAGAGAAATGGTTGTTGCGCTCAAGA 420  
 QY 421 AGAATGGAGCTGCAACGGCGTCTCGACTCTACTATGCGCAGAGAAAGCAATCTGTTTC 480

Db 421 AGAATGGAGCTGCAACGGCGTCTCGACTCTACTATGCGCAGAGAAAGCAATCTGTTTC 480  
 QY 481 TCCCTCGCGAGTCTCTCTGATTAAGAGATCTGTTCTGTTGACCACTCCAGAGAA 540  
 Db 481 TCCCTCGCGAGTCTCTCTGATTAAGAGATCTGTTCTGTTGACCACTCCAGAGAA 540  
 QY 541 GTTTCGAGGGTCTCTACCTGCTGACCCCAAAATGTTCCCTTGACCACTTGCTGCGCT 600  
 Db 541 GTTTCGAGGGTCTCTACCTGCTGACCCCAAAATGTTCCCTTGACCACTTGCTGCGCT 600  
 QY 601 AACCCCGCCGACAGAGCTGAAATTTGTAAGCACTT 638  
 Db 601 AACCCCGCCGACAGAGCTGAAATTTGTAAGCACTT 638  
 RESULT 3  
 AAT37503  
 ID AAT37503 standard; DNA; 638 BP.  
 XX AC AAT37503;  
 XX 25-MAR-2003 (revised)  
 DT 29-DEC-1996 (first entry)  
 XX Human beta-endothelial cell growth factor.  
 XX Endothelial cell growth factor; ECGF; blood vessel; regeneration;  
 KW heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;  
 KW fibroblast growth factor; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH CDS 39..506 /tag= a  
 FT misc\_RNA 42..503 /tag= b  
 FT /label= beta-ECGF  
 FT misc\_RNA 84..503 /tag= c  
 FT /label= acidic\_FGF  
 FT misc\_RNA 102..503 /tag= d  
 FT /label= alpha-ECGF  
 US5552528-A.  
 03-SEP-1996.  
 03-NOV-1994; 94US-00334884.  
 03-MAR-1986; 86US-00835594.  
 18-DEC-1987; 87US-00134499.  
 29-APR-1991; 91US-00693079.  
 27-NOV-1991; 91US-00799859.  
 (RHON ) RHONE POULENC RORER PHARM INC.  
 Maciag T, Burgess W;  
 WPI; 1996-412132/41.  
 P-PSDB; AAW04805, AAW04806, AAW04807.  
 Isolated, purified, biologically active bovine beta endothelial cell growth factor - useful to regenerate or treat damaged blood vessels.  
 Disclosure; Fig 8; 28pp; English.  
 Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a mol.wt. of 20 kD can be purified at least 16300 fold from bovine brain using heparin-Sepharose affinity chromatography. ECGF is useful for among other purposes, diagnostic applications and has potential in the treatment of damaged blood vessels or other endothelial cell-lined structures. Human ECGF (AAT37503) or fragments may be obtained using oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-2003 to correct PF field.)  
 Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;

[illegible]



AXX01723;  
20-APR-1999 (first entry)  
Human endothelial cell growth factor (ECGF) cDNA sequence.  
Endothelial cell growth factor; ECGF; cleavable; recombinant; repair;  
regenerate; blood vessel; endothelial cell; human; ss.  
Homo sapiens.

Key Location/Qualifiers  
CDS 39..506  
FT /\*tag= a  
FT /product= "ECGF"  
FT misc\_feature 42  
FT /\*tag= b  
FT /note= "beta-ECGF begins at this position"  
FT misc\_feature 84  
FT /\*tag= c  
FT /note= "acidic FGF begins at this position"  
FT misc\_feature 102  
FT /\*tag= d  
FT /note= "alpha-ECGF begins at this position"

US849538-A.  
15-DEC-1998.  
11-APR-1997; 97US-00840088.  
03-MAR-1986; 86US-00835594.  
18-DEC-1987; 87US-00134499.  
29-APR-1991; 91US-00693079.  
27-NOV-1991; 91US-00799859.  
03-NOV-1994; 94US-00334884.  
07-JUN-1995; 95US-00472964.  
04-NOV-1996; 96US-00743261.  
(RHON ) RHONE-POULENC RORER PHARM INC.

Jaye M, Burgess W, Maciag T, Drohan WN;  
WPI; 1999-069734/06.  
P-PSDB; AAW92291.  
DNA encoding a cleavable signal peptide and an endothelial cell growth  
factor - useful for producing recombinant endothelial cell growth factor  
proteins.  
Disclosure; Fig 8; 23pp; English.

The invention relates to DNA encoding human endothelial cell growth  
factors (ECGF) and plasmids comprising the DNA sequences. The DNA encodes  
a cleavable signal peptide and an ECGF, where removal of the signal  
peptide yields a mature form of the ECGF, where the ECGF is alpha-ECGF or  
beta-ECGF. The DNA is used to produce recombinant ECGF proteins, which  
can be used in treatments to repair or regenerate blood vessels or other  
structures lined with endothelial cells. The present sequence represents  
a human ECGF cDNA sequence (determined from lambda ECGF clones 1 and 29)

Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
Query Match 99.2%; Score 633.2; DB 2; Length 638;  
Best Local Similarity 99.5%; Pred. No. 3.5e-186;  
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTGGGAAACCGCCAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACCA 60  
DB 1 GAATTGGGAAACCGCCAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACCA 60  
QY 61 CTTTCACAGCCCTGACCGAGAGATTAAATCTGCTTCAGGGGAATTACAGAGCCCAAC 120  
DB 61 CTTTCACAGCCCTGACCGAGAGATTAAATCTGCTTCAGGGGAATTACAGAGCCCAAC 120  
QY 121 TCCTCTACTGTAGCAACGGGGGCCATCTTCCTGAGGATCTTCCTGGATGCACAGTGGATG 180  
DB 121 TCCTCTACTGTAGCAACGGGGGCCATCTTCCTGAGGATCTTCCTGGATGCACAGTGGATG 180

QY 181 GGACAGGCGACAGAGCGGACGACGACATTCAGCTGCGAGTCTAGTGGGGAAGCGTGGGG 240  
DB 181 GGACAGGCGACAGAGCGGACGACGACATTCAGCTGCGAGTCTAGTGGGGAAGCGTGGGG 240  
QY 241 AGCTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGCTTT 300  
DB 241 AGCTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGCTTT 300  
QY 301 TATAGGCTCAGACAGACCAATGAGGAATGTTTCTGGAAGGCTGGAGGAGAC 360  
DB 301 TATAGGCTCAGACAGACCAATGAGGAATGTTTCTGGAAGGCTGGAGGAGAC 360  
QY 361 ATTACACACCTATATATCCAAAGAGCATGACAGAGAATTTGGTTTGGGCTCAAGA 420  
DB 361 ATTACACACCTATATATCCAAAGAGCATGACAGAGAATTTGGTTTGGGCTCAAGA 420  
QY 421 AGAATGGAGCTGCAACGGGCTCTCGGACTCACTATGGCCAAAAGCAATCTTTTTC 480  
DB 421 AGAATGGAGCTGCAACGGGCTCTCGGACTCACTATGGCCAAAAGCAATCTTTTTC 480  
QY 481 TCCCTCTCCAGTCTCTCTGATTAAAGAGATCTGTTCTGTGTGACCACTCCAGAA 540  
DB 481 TCCCTCTCCAGTCTCTCTGATTAAAGAGATCTGTTCTGTGTGACCACTCCAGAA 540  
QY 541 GTTTCGAGGGTCTCTGCTGGTGTGACCCCAAAATGTTCCCTGACCAITGGCTGGCT 600  
DB 541 GTTTCGAGGGTCTCTGCTGGTGTGACCCCAAAATGTTCCCTGACCAITGGCTGGCT 600  
QY 601 AACCCCGACGACGAGCTGAAATTTGTAGCAACTT 638  
DB 601 AACCCCGACGACGAGCTGAAATTTGTAGCAACTT 638

RESULT 6  
ACF04028  
ID ACF04028 standard; DNA; 638 BP.  
XX AC ACF04028;  
XX AC ACF04028;  
DT 15-OCT-2003 (first entry)  
XX DE Thrombin resistant FGF-1 mutant production wildtype coding sequence.  
XX KW Thrombin resistant FGF-1; FGF-1; fibroblast growth factor-1;  
KW myocardial ischaemia; peripheral vascular disease; cerebral ischaemia;  
KW epithelial injury; epidermal wound injury; nerve injury; bone damage;  
KW vasotropic; cardiant; cerebroprotective; vulnerary; neuroprotective;  
KW osteopathic; gene; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 42..506  
FT /\*tag= a  
FT /product= "FGF-1"  
FT /partial  
FT /note= "no start codon"  
XX WC2003052378-A2.  
XX PD 26-JUN-2003.  
XX PF 11-DEC-2002; 2002WO-US039686.  
XX PR 17-DEC-2001; 2001US-00022554.  
XX XX (REPA-) REPAIR INC.  
XX PA (MAIN-) MAINE MEDICAL CENT RES INST.  
XX PI Maciag T, Ettenson DS, Burgess WH, Drohan WN;  
XX WPI; 2003-559052/52.  
XX DR P-PSDB; ABR63868.  
XX PT New thrombin degradation resistant fibroblast growth factor-1 (FGF-1)  
PT polypeptide, useful for treating a disease or disorder, e.g. cerebral  
PT ischemia or bone damage, or for enhancing the effectiveness of an FGF-1  
PT response in a mammal.  
XX

PS Claim 2; Fig 8; 83pp; English.

XX The present invention provides the protein and coding sequences of human  
CC fibroblast growth factor-1 (FGF-1) and a mutant that is resistant to  
CC thrombin degradation. The thrombin degradation resistant FGF-1 protein  
CC can be used for treating a disease or disorder (e.g. myocardial  
CC ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial  
CC injury, epidermal wound injury, nerve injury, or bone damage), for  
CC enhancing the effectiveness of an FGF-1 response, or for stimulating an  
CC FGF-1 response in a mammal. The present sequence is the wildtype FGF-1  
CC coding sequence

XX SQ Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;

Query Match 99.2%; Score 633.2; DB 8; Length 638;  
Best Local Similarity 99.5%; Pred. No. 3.5e-186;  
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTCGGAGCGCCGACACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAATCACCA 60  
Db 1 GAATTCGGAGCGCCGACACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAATCACCA 60  
QY 61 CTTTCACAGCCCTGACCGAGAGTTTAAATCTGCTCCAGCGAATTACAGAGCCCAAC 120  
Db 61 CTTTCACAGCCCTGACCGAGAGTTTAAATCTGCTCCAGCGAATTACAGAGCCCAAC 120  
QY 121 TCTCTACTGTAGCAAGGGGGCCACTTCTGAGATGCTTCGGATGGCACAGTGATG 180  
Db 121 TCTCTACTGTAGCAAGGGGGCCACTTCTGAGATGCTTCGGATGGCACAGTGATG 180  
QY 181 GGACAAAGGACGAGGAGCGACACACATTCAGCTCGAGCTCAGTCCGGAAGCGTGGGG 240  
Db 181 GGACAAAGGACGAGGAGCGACACATTCAGCTCGAGCTCAGTCCGGAAGCGTGGGG 240  
QY 241 AGTGTTATTAAGAGTACGAGAGTGGCGAGTCTGGCGATGACACCGAGCGGCTTT 300  
Db 241 AGTGTTATTAAGAGTACGAGAGTGGCGAGTCTGGCGATGACACCGAGCGGCTTT 300  
QY 301 TATAGCGCTCACAGACCAATGAGGAATGTTTGTCTCGAAAGGCTCGAGAGAAC 360  
Db 301 TATAGCGCTCACAGACCAATGAGGAATGTTTGTCTCGAAAGGCTCGAGAGAAC 360  
QY 361 ATTACACACCTATATATCCAGAGCATGCGAGAGAAATGTTTGTGGCTCAAGA 420  
Db 361 ATTACACACCTATATATCCAGAGCATGCGAGAGAAATGTTTGTGGCTCAAGA 420  
QY 421 AGAATGGAGCTGCAACCGGCTCTCTAAACTCACTATGCCAGAAAGCAATCTGTTC 480  
Db 421 AGAATGGAGCTGCAACCGGCTCTCTAAACTCACTATGCCAGAAAGCAATCTGTTC 480  
QY 481 TCCGCTCCGAGTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACACTCCAGAA 540  
Db 481 TCCGCTCCGAGTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACACTCCAGAA 540  
QY 541 GTTTCGAGGGTCTCACTGCTGCTGACCCCAAAATGTTCCCTGACCATTTGGCTGCCT 600  
Db 541 GTTTCGAGGGTCTCACTGCTGCTGACCCCAAAATGTTCCCTGACCATTTGGCTGCCT 600  
QY 601 AACCCGAGCCGACAGAGCTGAATTTGTAAGCACTT 638  
Db 601 AACCCGAGCCGACAGAGCTGAATTTGTAAGCACTT 638

RESULT 7

AAT45985

ID AAT45985 standard; cDNA; 639 BP.

XX AC AAT45985;

XX 25-MAR-2003 (revised)

DT 17-MAR-1997 (first entry)

XX Human endothelial cell growth factor cDNA.

XX Endothelial cell growth factor; ECGF; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

CDS 1..507  
/\*tag= a

XX US5571790-A.  
XX 05-NOV-1996.  
XX 07-JUN-1995; 95US-00472964.  
XX 03-MAR-1986; 86US-00835594.  
XX 18-DEC-1987; 87US-00134499.  
XX 29-APR-1991; 91US-00693079.  
XX 27-NOV-1991; 91US-00799859.  
XX 03-NOV-1994; 94US-00334884.

XX (RHON ) RHONE POULENC RORER PHARM INC.

XX Drohan WN, Jaye M, Maciag T, Burgess W;

XX WPI; 1996-505421/50.

XX P-PSDB; AAN06818.

XX Recombinant human endothelial cell growth factors - for treating damaged  
XX blood vessels, etc.

XX Example D; Fig 8; 22pp; English.

XX A cDNA clone (AAT45985) codes for human endothelial cell growth factor  
XX (AAN06818). To obtain the clone, a human brain stem cDNA library was  
XX screened with a probe (see also AAT45986) based on N-terminal sequences  
XX of bovine ECGF (see also AAN06819-20). ECGF clones 1 and 29 were  
XX isolated, subcloned into M13mp8 and the ECGF open reading frame and  
XX flanking regions sequenced by the chain termination method. DNA sequences  
XX (see also AAT45983-84) derived from the complete cDNA can be used in the  
XX large-scale prodn. of recombinant ECGF beta (AAN06816) and alpha  
XX (AAN06817) in transformed host cells. (Updated on 25-MAR-2003 to correct  
XX PF field.)

XX SQ Sequence 639 BP; 172 A; 165 C; 168 G; 134 T; 0 U; 0 Other;

Query Match 97.5%; Score 622.2; DB 2; Length 639;

Best Local Similarity 99.4%; Pred. No. 9.3e-183;

Matches 635; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAATTCGGAGCGCCGACACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAATCACCC 59  
Db 1 GAATTCGGAGCGCCGACACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAATCACCC 60  
QY 60 ACCTTCACAGCCCTGACCGAGAGTTTAAATCTGCTCCAGCGAATTACAGAGCCCAAA 119  
Db 61 ACCTTCACAGCCCTGACCGAGAGTTTAAATCTGCTCCAGCGAATTACAGAGCCCAAA 120  
QY 120 CTCCTCTACTGTAGCAACGGGGGCCACTTCTCGAGGATCTTCGGATGGCACAGTGGAT 179  
Db 121 CTCCTCTACTGTAGCAACGGGGGCCACTTCTCGAGGATCTTCGGATGGCACAGTGGAT 180  
QY 180 GGGACAGGACGAGGAGCGACAGCACAATTCAGCTCGAGCTCAGTGGGAAAGCTGGGG 239  
Db 181 GGGACAGGACGAGGAGCGACAGCACAATTCAGCTCGAGCTCAGTGGGAAAGCTGGGG 240  
QY 240 GAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGACACCGAGCGCTT 299  
Db 241 GAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGACACCGAGCGCTT 300  
QY 300 TTATAGCGCTCACACACCAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGAGAAC 359  
Db 301 TTATAGCGCTCACACACCAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGAGAAC 360  
QY 360 CATTACACACCTTATATATCCAGAGCATGCGAGAGAAATGTTTGTTCCTCAAG 419  
Db 361 CATTACACACCTTATATATCCAGAGCATGCGAGAGAAATGTTTGTTCCTCAAG 420  
QY 420 AGAATGGAGCTGCAACCGGCTCTCTAAACTCACTATGGCCAGAAAGCAATCTGTTC 479  
Db 421 AGAATGGAGCTGCAACCGGCTCTCTAAACTCACTATGGCCAGAAAGCAATCTGTTC 480  
QY 480 CTCGCCCTGCGAGTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACACTCCAGAGA 539  
Db 481 CTCGCCCTGCGAGTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACACTCCAGAGA 540

QY 540 AGTTTCAGGGGTCTCCTCAGCTGTGACCCAAATGTTCCCTTGACCAATGGCTGGCG 599  
Db 541 AGTTTCAGGGGTCTCCTCAGCTGTGACCCAAATGTTCCCTTGACCAATGGCTGGCG 600  
QY 600 TAAACCCCGCCAGAGAGCTGTAATTTGTAAGCAACTT 638  
Db 601 TAAACCCCGCCAGAGAGCTGTAATTTGTAAGCAACTT 639  
RESULT 8  
ACC42968  
ID ACC42968 standard; DNA; 2357 BP.  
XX  
AC ACC42968;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
DE Human Fibroblast Growth Factor 1 coding sequence.  
XX  
KW Human; Fibroblast Growth Factor 1; FGF1; acidic FGF; aFGF;  
KW acidic Fibroblast Growth Factor; protein co-ordinate data; gene; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 142..609  
XX FT /\*tag= a  
XX FT /product= "FGF1"  
XX  
XX W02003038054-A2.  
XX  
XX PD 08-MAY-2003.  
XX  
XX EF 31-OCT-2002; 2002MO-US034986.  
XX  
XX PR 31-OCT-2001; 2001US-0335583P.  
XX  
XX PA (UZYNY ) UNIV NEW YORK STATE.  
XX  
XX PI Moosa M, Green DL, Linhard RV;  
XX  
XX DR WPI; 2003-482144/45.  
XX  
XX DR P-PSDB; ABR56165.  
XX  
XX PT Composition useful for identifying modulators of fibroblast growth factor  
XX -mediated signaling for use in treating cancer, has ternary complex of  
XX FGF-receptor, FGF ligand and heparin agonist or antagonist.  
XX  
XX PS Disclosure; Fig 16B; 288pp; English.  
XX  
XX CC The present invention relates to an isolated composition comprising a  
XX ternary complex of an Fibroblast Growth Factor (FGF) ligand polypeptide  
XX (ABR56163, ABR56165), an FGF receptor polypeptide (ABR56164) and a  
XX heparin agonist or antagonist, where the agonist or antagonist binds to  
XX the FGF ligand polypeptide and the FGF receptor polypeptide to form the  
XX ternary complex. The composition is useful for identifying a compound  
XX that is an inhibitor of FGF receptor activity. FGF1 is also known as  
XX acidic FGF  
XX  
SQ Sequence 2357 BP; 691 A; 521 C; 567 G; 578 T; 0 U; 0 Other;  
Query Match 94.3%; Score 601.8; DB 9; Length 2357;  
Best Local Similarity 98.6%; Pred. No. 3.8e-176;  
Matches 628; Conservative 0; Mismatches 7; Indels 2; Gaps 2;  
QY 3 ATTGCGGAGCGGCCAAGCAGAGCTGCTGAGCATGCTGAGGGGAAATCAACACC 62  
Db 106 AGTCTTGAAGGGCCCAAGCAGAGCTGCTGAGCATGCTGAGGGGAAATCAACACC 165  
QY 63 TTCACGCTCAGCGAGAGTTAATCTGCTCCAGGGAATTCAGAGAGCCCAATCTC 122  
Db 166 TTCACGCTCAGCGAGAGTTAATCTGCTCCAGGGAATTCAGAGAGCCCAATCTC 225  
QY 123 CTCTACTGTAGCAACGGGGGCCCACTTCTCTGAGGATCTTCGCGATGCGACGTGGATGGG 182  
Db 226 CTCTACTGTAGCAACGGGGGCCCACTTCTCTGAGGATCTTCGCGATGCGACGTGGATGGG 285  
QY 183 ACAAGGGACAGAGCGCAGCAGCAATTCAGCTGAGCTAGTGGCGGAAGCGTGGGGGAG 242

Db 286 ACNAGGACAGGCGACCGACCACTTCAGCTGCGAGCTCAGTCCGGAAGCGTGGGGAG 345  
QY 243 GTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGGCTTTTA 302  
Db 346 GTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGGCTTTTA 405  
QY 303 TACGGCTCACAGACACCAATAGGAAATGTTCTTCTGGAAGGCTGGAGGAGCACT 362  
Db 406 TACGGCTCACAGACACCAATAGGAAATGTTCTTCTGGAAGGCTGGAGGAGCACT 465  
QY 363 TACAACACTTATATATCAAGAAGCATGAGAGAGATGTTTGTGGCTCTCAAGAG 422  
Db 466 TACAACACTTATATATCAAGAAGCATGAGAGAGATGTTTGTGGCTCTCAAGAG 525  
QY 423 AATGGAGCTGCAACCGGCTCTTAACACTCACTATGCCAGAGAGCAATCTGTCTCTC 482  
Db 526 AATGGAGCTGCAACCGGCTCTCGACTCACTATGCCAGAGAGCAATCTGTCTCTC 585  
QY 483 CCGCTGGCAGTCTCTCTGATTAAGAAGATCTGTCTCT -GGTGTTCACCTCCAGAGAG 541  
Db 586 CCGCTGGCAGTCTCTCTGATTAAGAAGATCTGTCTCTGGGTGTTCACCTCCAGAGAG 645  
QY 542 TTTCGAGGGGTCTCTCACTGCTGTGACCCCAAAATGTTCCCTTGACCAATGGCTGGCTA 601  
Db 646 TTTCGAGGGGTCTCTCACTGCTGTGACCCCAAAATGTTCCCTTGACCAATGGCTGGCTA 704  
QY 602 ACCCCAGCCACAGAGCGCTGAAATTTGTAAGCAACTT 638  
Db 705 ACCCCAGCCACAGAGCGCTGAAATTTGTAAGCAACTT 741  
RESULT 9  
ABX63225  
ID ABX63225 standard; cDNA; 4087 BP.  
XX  
AC ABX63225;  
XX  
XX 25-FEB-2003 (first entry)  
XX  
XX Human cDNA #225 differentially expressed in activated vascular tissue.  
XX  
XX Human; Gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;  
XX hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;  
XX gene therapy; vascular disease; cancer; coronary; artery disease;  
XX hypertension; diabetes; pre-eclampsia; restenosis;  
XX ischaemia-reperfusion injury; stroke.  
XX  
XX OS Homo sapiens.  
XX  
XX FN US2002137081-A1.  
XX  
XX PD 26-SEP-2002.  
XX  
XX PP 08-JAN-2002; 2002US-00044090.  
XX  
XX XX 28-JUL-2000; 2000US-0222469P.  
XX  
XX PR 08-JAN-2001; 2001US-0260483P.  
XX  
XX PA (BAND/) BANDMAN O.  
XX  
XX PI Bandman O;  
XX  
XX DR WPI; 2003-110597/10.  
XX  
XX PT Combination for diagnosing, staging, treating, or monitoring the  
XX progression of treatment of a vascular disease, e.g. atherosclerosis,  
XX comprises several cDNAs that are differentially expressed in activated  
XX vascular tissue.  
XX  
XX PS Claim 1; Page; 18pp; English.  
XX  
XX CC This invention relates to a combination comprising several cDNAs that are  
XX differentially expressed in activated vascular tissue. The invention also  
XX discloses a high throughput method for detecting differentially expressed  
XX cDNAs in a sample. The cDNAs of the invention may have  
XX antiatherosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;  
XX gynaecological; vasotropic and cerebroprotective activities and may be  
XX used in gene therapy. The cDNAs of the invention may be used in a high-

CC throughput methods for detecting differential expression of one or more  
CC cDNAs in a sample, or screening several molecules or compounds to  
CC identify a molecule or compound that specifically binds a cDNA of the  
CC invention. A protein encoded by the cDNA may be used to screen several  
CC molecules or compounds to identify a ligand that specifically binds to  
CC the protein, or to produce or purify an antibody to the protein that can  
CC be used to detect a protein in a sample or purify a natural or  
CC recombinant protein from a sample. The nucleotides may be useful for  
CC diagnosing, staging, treating, or monitoring the progression of treatment  
CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery  
CC disease, hypertension, diabetes, pre-eclampsia, ischaemia- reperfusion  
CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale  
CC genetic or gene expression analysis of several new nucleic acid  
CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for  
CC diagnosing pre-pathologic disorders, and chronic or acute diseases  
CC associated with abnormalities in the expression, amount or distribution  
CC of the protein. The present sequence represents a cDNA of the invention  
CC that is differentially expressed in activated vascular tissue. Note: The  
CC sequence data for this patent did not form part of the specification, but  
CC was obtained in electronic format directly from USPTO at  
CC <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>  
XX  
XX  
SQ Sequence 4087 BP; 1164 A; 886 G; 959 C; 1078 T; 0 U; 0 Other;

Query Match 94.3%; Score 601.8; DB 7; Length 4087;  
Best Local Similarity 98.6%; Pred. No. 4.9e-176;  
Matches 628; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGACGGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCAC 62  
Db 470 AGTCTTGAAGGCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCAC 529  
QY 63 TTCACGCGCTCAGCGAGAGTTTAATCTGCTCCGCGGAAATACAGAGCCCAACTC 122  
Db 530 TTCACGCGCTCAGCGAGAGTTTAATCTGCTCCGCGGAAATACAGAGCCCAACTC 589  
QY 123 CTCTACTGTAGCAACGCGGGCCACTTCTCGAGGATCTTCCGGATGCGCAGTGGATGGG 182  
Db 590 CTCTACTGTAGCAACGCGGGCCACTTCTCGAGGATCTTCCGGATGCGCAGTGGATGGG 649  
QY 183 ACAGGGACGAGGCGACAGCAGCATTACCTGAGCTGAGTGGGATGCGCAGTGGATGGG 242  
Db 650 ACAGGGACGAGGCGACAGCAGCATTACCTGAGCTGAGTGGGATGCGCAGTGGATGGG 709  
QY 243 GTGTATATAAGAGTACCGGAGCTGGCCAGTACTTGGCCATGCGCAGTGGATGGG 302  
Db 710 GTGTATATAAGAGTACCGGAGCTGGCCAGTACTTGGCCATGCGCAGTGGATGGG 769  
QY 303 TACGCTCAGCAGCAGCAGCAGCAGTGGTCTGCGGATGCGCAGTGGATGGG 362  
Db 770 TACGCTCAGCAGCAGCAGCAGCAGTGGTCTGCGGATGCGCAGTGGATGGG 829  
QY 363 TACACACCTTATATATCAAGAGCAGTGGATGGTCTGCGGATGCGCAGTGGATGGG 422  
Db 830 TACACACCTTATATATCAAGAGCAGTGGATGGTCTGCGGATGCGCAGTGGATGGG 889  
QY 423 AATGGAGCTGCAACCGGCTCTAAGCTCAGTGGATGGTCTGCGGATGCGCAGTGGATGGG 482  
Db 890 AATGGAGCTGCAACCGGCTCTAAGCTCAGTGGATGGTCTGCGGATGCGCAGTGGATGGG 949  
QY 483 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCT- GGTGTGACCACTCCAGAGAG 541  
Db 950 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCTGCGGATGCGCAGTGGATGGG 1009  
QY 542 TTTCAGGGGCTCCTCAGTGGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGG 601  
Db 1010 TTTCAGGGGCTCCTCAGTGGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGG 1068  
QY 602 ACCCCAGCCACAGAGCTGAAATTTGAGCAACTT 638  
Db 1069 ACCCCAGCCACAGAGCTGAAATTTGAGCAACTT 1105

RESULT 10  
ID AAN93088  
XX AAN93088 standard; DNA; 638 BP.  
XX  
XX AAN93088;

DT 25-MAR-2003 (revised)  
DT 25-JUN-1990 (first entry)  
XX Acidic fibroblast growth factor.  
DE Acidic fibroblast growth factor.  
KW Acidic fibroblast growth factor; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT mat\_peptide 91..555  
FT /\*tag= a  
FT /label= human acidic fibroblast growth factor  
XX  
XX EF298723-A.  
XX  
XX 11-JAN-1989.  
XX  
XX 06-JUL-1988; 88EP-00306158.  
XX  
XX 07-JUL-1987; 87US-00070797.  
XX  
XX (BIOU ) BIOTECH RES INST.  
XX  
XX Fiddes JC, Abraham JA, Protter A;  
XX WPI; 1989-009785/02.  
XX N-PSDB; AAN93087.  
XX  
XX Recombinant DNA encoding new fibroblast growth factor analogues - useful  
XX e.g. for accelerating wound healing and to control neovascularisation.  
XX  
XX Disclosure; Fig 2; 44pp; English.

CC The sequence encodes human acidic fibroblast growth factor (aFGF). See  
CC also AAN93087 and AAN93089. (Updated on 25-MAR-2003 to correct PA field.)  
XX  
XX Sequence 638 BP; 170 A; 156 G; 168 C; 144 T; 0 U; 0 Other;

Query Match 86.2%; Score 549.8; DB 1; Length 638;  
Best Local Similarity 98.5%; Pred. No. 3e-160;  
Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGACGGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCAC 62  
Db 55 AGTCTTGAAGGCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCAC 114  
QY 63 TTCACGCGCTCAGCGAGAGTTTAATCTGCTCCGCGGAAATACAGAGCCCAACTC 122  
Db 115 TTCACGCGCTCAGCGAGAGTTTAATCTGCTCCGCGGAAATACAGAGCCCAACTC 174  
QY 123 CTCTACTGTAGCAACGCGGGCCACTTCTCGAGGATCTTCCGGATGCGCAGTGGATGGG 182  
Db 175 CTCTACTGTAGCAACGCGGGCCACTTCTCGAGGATCTTCCGGATGCGCAGTGGATGGG 234  
QY 183 ACAGGGACGAGGCGACAGCAGCATTACCTGAGCTGAGTGGGATGCGCAGTGGATGGG 242  
Db 235 ACAGGGACGAGGCGACAGCAGCATTACCTGAGCTGAGTGGGATGCGCAGTGGATGGG 294  
QY 243 GTGTATATAAGAGTACCGGAGCTGGCCAGTACTTGGCCATGCGCAGTGGATGGG 302  
Db 295 GTGTATATAAGAGTACCGGAGCTGGCCAGTACTTGGCCATGCGCAGTGGATGGG 354  
QY 303 TACGCTCAGCAGCAGCAGCAGTGGTCTGCGGATGCGCAGTGGATGGG 362  
Db 355 TACGCTCAGCAGCAGCAGCAGTGGTCTGCGGATGCGCAGTGGATGGG 414  
QY 363 TACACACCTTATATATCAAGAGCAGTGGATGGTCTGCGGATGCGCAGTGGATGGG 422  
Db 415 TACACACCTTATATATCAAGAGCAGTGGATGGTCTGCGGATGCGCAGTGGATGGG 474  
QY 423 AATGGAGCTGCAACCGGCTCTAAGCTCAGTGGATGGTCTGCGGATGCGCAGTGGATGGG 482  
Db 475 AATGGAGCTGCAACCGGCTCTAAGCTCAGTGGATGGTCTGCGGATGCGCAGTGGATGGG 534  
QY 483 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCT- GGTGTGACCACTCCAGAGAG 541  
Db 535 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCTGCGGATGCGCAGTGGATGGG 594

QY 542 TTTCGAGGGTCTCACTGCTGAGCCCAAAATGTTCCCTTGA 586  
DB 595 TTTCGAGGGTCTCACTGCTGAG-CCCAAAATGTTCCCTTGA 638

RESULT 11

AAT12907  
ID AAT12907 standard; cDNA; 8501 BP.  
XX  
AC AAT12907;  
XX  
DT 05-NOV-1996 (first entry)  
XX  
DE Novel expression plasmid pXL2435.  
XX  
KW Expression vector; T7 phage; gene 10; promoter; heterologous; circular;  
transcriptional terminator; plasmid stability region; RP4; maintenance;  
plasmid loss; antibiotic resistance; selection; pharmaceutical;  
KW agricultural; biocatalysis; ds.  
XX  
OS Synthetic.

XX Key Location/Qualifiers  
FH misc\_feature 6038..8499  
FT /\*tag= a  
FT /notes "contains sequence derived from par region of  
FT plasmid RP4"

XX MO9608572-A1.  
XX 21-MAR-1996.  
XX 14-SEP-1995; 95WO-FR001178.  
XX 16-SEP-1994; 94FR-00011049.  
XX (RHON) RHONE POULENC RORER SA.  
XX Cameron B, Crouzet J;  
XX WPI; 1996-179946/18.  
XX Expression plasmids contg. phage T7 promoter - and stabilising par region  
from plasmid RP4.  
XX Claim 11; Page 14-19; 35pp; French.

XX This is the nucleotide sequence of a novel expression plasmid derived  
from the pET series of expression vectors. The plasmid retains the T7  
heterologous proteins e.g. basic fibroblast growth factor. The novelty of  
the plasmid derives from the inclusion of the plasmid stability region of  
plasmid RP4. This region allows maintenance of the plasmid and prevents  
plasmid loss without the need for antibiotic resistance genes for  
selection and maintenance. The RP4 par region comprises the genes parA,  
B, C, D and E. They are placed in the plasmid under control of the lacO  
operator and lacI(q) repressor. The novel plasmid can be used to express  
proteins of pharmaceutical, agricultural or biocatalytic interest without  
the use of antibiotics in the culture medium which, when present in trace  
amounts in final preparations, could lead to undesired side effects or  
antibiotic resistant microorganisms flourishing

XX Sequence 8501 BP; 1862 A; 2422 C; 2426 G; 1791 T; 0 U; 0 Other;

Query Match 73.8%; Score 470.6; DB 2; Length 8501;  
Best Local Similarity 99.2%; Pred. No. 4.3e-135;  
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAATCTGCTCCA 98  
DB 108 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAATCTGCTCCA 167  
QY 99 GGGAAATTACAGAGCCGAAATCTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 158  
DB 168 GGGAAATTACAGAGCCGAAATCTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 227  
QY 159 CTTCCGATGGCAGCATGTGATGGGACAGGAGGACAGGAGGACACCATTCAGCTGACG 218  
DB 228 CTTCCGATGGCAGCATGTGATGGGACAGGAGGACAGGAGGACACCATTCAGCTGACG 287

QY 219 CTCAGTGGGAAAGCGTGGGGAGGTGTATATTAAGAGTACCGAGACTGGCCAGTACTTG 278  
DB 288 CTCAGTGGGAAAGCGTGGGGAGGTGTATATTAAGAGTACCGAGACTGGCCAGTACTTG 347  
QY 279 GCCATGACACCGACGGGCTTTTATACGGCTTCACAGACCAAAATGAGGAATGTTGTTTC 338  
DB 348 GCCATGACACCGACGGGCTTTTATACGGCTTCACAGACCAAAATGAGGAATGTTGTTTC 407  
QY 339 CTGGAAGGCTGGAGGAGACCAATTACACCTATATATCCAGAGCATGCGAGAGAG 398  
DB 408 CTGGAAGGCTGGAGGAGACCAATTACACCTATATATCCAGAGCATGCGAGAGAG 467  
QY 399 AATTGTTTGTGTGGCTTCAAGGAAGATGGAGCTGCAAAACGGGTCCTAAAACTCACTAT 458  
DB 468 AATTGTTTGTGTGGCTTCAAGGAAGATGGAGCTGCAAAACGGGTCCTCGAGCTCACTAT 527  
QY 459 GGCAGAAAGCAATCTGTTTCTCCCTGCGAGTCTTCTGATTAAGAGATCTG 515  
DB 528 GGCAGAAAGCAATCTGTTTCTCCCTGCGAGTCTTCTGATTAAGAGATCTG 584

RESULT 12

AAN71029  
ID AAN71029 standard; DNA; 481 BP.  
XX  
AC AAN71029;  
XX  
DT 18-APR-1991 (first entry)  
XX  
DE Sequence of partially synthetic gene for human acidic fibroblast growth  
factor (FGF).

XX Wound healing; tissue repair; tumour probe; ds.

XX Homo sapiens.

XX WO8701728-A.

XX 26-MAR-1987.

XX 11-SEP-1986; 86WO-US001879.

XX 12-SEP-1985; 85US-00775521.

XX 16-DEC-1985; 85US-00809163.

XX 30-MAY-1986; 86US-00869382.

XX (BIOT-) BIOTECHN RES PARTNE.

XX Fiddes JC, Abraham JA;

XX WPI; 1987-093786/13.

XX New DNA sequences encoding mammalian fibroblast growth factors - useful  
in prodn. of pure factors for use in wound healing and tissue repair and  
of probe for tumour testing.

XX Example; Fig 9; 89pp; English.

XX The N-terminal AA sequence of both acidic and basic bovine FGF are used  
to construct long probes to screen human and bovine genomic libraries for  
CC FGF genes. Isolated sequences are used in vector construction etc. and  
CC used to transform CV-1 cells for FGF prodn

XX Sequence 481 BP; 133 A; 118 C; 129 G; 101 T; 0 U; 0 Other;

Query Match 72.7%; Score 464; DB 1; Length 481;  
Best Local Similarity 98.9%; Pred. No. 1.2e-133;  
Matches 467; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 37 CCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAATCTGCTTC 96  
DB 1 CCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAATCTGCTTC 60  
QY 97 CAGGGAATTACAGAGGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTCTGAGGA 156  
DB 61 CAGGGAATTACAGAGGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTCTGAGGA 120  
QY 157 TCCTCCGGATGGCAGTGGATGGGACAGGAGGACAGGAGGACAGCATTCACGTGC 216

Db 121 TCCTTCGGATGCGACAGTGGATGGGCAAGGCGACAGGAGCGACACAGCATTCAGCTGC 180  
 QY 217 AGCTCAGTGGCGAAGACGCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCGAGTACT 276  
 Db 191 AGCTCAGTGGCGAAGACGCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCGAGTACT 240  
 QY 277 TGGCCATGCGACCGGACCGGCTTTTATACGGCTCACAGACCAAAATGAGGAATGTTTGT 336  
 Db 241 TGGCTATGCGACCGGACCGGCTTTTATACGGCTCACAGACCAAAATGAGGAATGTTTGT 300  
 QY 337 TCTTGGAAAGGCTGGAGGAGACCAATACACACTATATATCCAGAGCATGCAGAGA 396  
 Db 301 TCTTGGAAAGGCTGGAGGAGACCAATACACACTATATATCCAGAGCATGCAGAGA 360  
 QY 397 AGAATGTGTTGTGTGGCTCAAGGAATGGAGCTGCAACCGCGTCTCTAAACTCACT 456  
 Db 361 AGAATGTGTTGTGTGGCTCAAGGAATGGAGCTGCAACCGCGTCTCTCGACTCACT 420  
 QY 457 ATGGCCAGAAAGCAATCTTGTTCCTCCCTGCGAGTCTCTTCTGATTAAG 508  
 Db 421 ATGGCCAGAAAGCAATCTTGTTCCTCCCTGCGAGTCTCTTCTGATTAAG 472  
 RESULT 13  
 AAN90994  
 ID AAN90994 standard; DNA; 481 BP.  
 XX  
 AC AAN90994;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-JUN-1990 (first entry)  
 XX  
 DE Partially synthetic nucleotide sequence encoding human acidic fibroblast growth factor (haFGF).  
 DE  
 XX Human acidic fibroblast growth factor; synthetic gene; lambda HAG-9.1;  
 KW pAL12-haFGF; pAL13-haFGF; E. coli r3 promoter.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature complement(1..122)  
 FT /tag= b  
 FT /note= "As above"  
 FT 1..118  
 FT /tag= a  
 FT /note= "from genomic lambda HAG-9.1 clone"  
 FT 3..5  
 FT /tag= w  
 FT /note= "Believed to be the start codon for pro sequence of haFGF"  
 FT 119..154  
 FT /tag= c  
 FT /note= "oligo 1"  
 FT complement(123..158)  
 FT /tag= d  
 FT /note= "oligo 11"  
 FT 155..190  
 FT /tag= e  
 FT /note= "oligo 2"  
 FT complement(159..194)  
 FT /tag= f  
 FT /note= "oligo 12"  
 FT 191..226  
 FT /tag= g  
 FT /note= "oligo 3"  
 FT complement(195..230)  
 FT /tag= h  
 FT /note= "oligo 13"  
 FT 230..262  
 FT /tag= i  
 FT /note= "oligo 4"  
 FT complement(231..266)  
 FT /tag= j  
 FT /note= "oligo 14"  
 FT complement(245)  
 FT /tag= x  
 FT /note= "Differs from haFGF cDNA sequence of Jaye et al in

which this base was G. "  
 245  
 /tag= x  
 /note= "Differs from haFGF cDNA sequence of Jaye et al in which this base was C."  
 263..299  
 /tag= k  
 /note= "oligo 5"  
 complement(267..303)  
 /tag= l  
 /note= "oligo 15"  
 300..334  
 /tag= m  
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 /note= "oligo 7"  
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 371..406  
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 407..442  
 /tag= s  
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 complement(411..446)  
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 443..476  
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 WO8902471-A.  
 23-MAR-1989.  
 02-SEP-1988; 88WO-US003080.  
 11-SEP-1987; 87US-00095742.  
 (CALD ) CALIFORNIA BIOTECHNOLOGY INC.  
 Talmadge KD, Hilliker S;  
 MPI; 1989-100011/13.  
 DNA constructs contg. R3 promoter from E. coli - having high strength and being insensitive to catabolite repression.  
 Fig 10; Page 7; 70pp; English.  
 This sequence is referred to in the spec. as both Figure 10 and Figure 11. The 5' portion of the gene was provided by genomic lambda HAG-9.1 clone. This portion encodes the 15 amino acids of the pro sequence along with the first 25 amino acids of the mature 'primary' form of haFGF. The remainder was constructed from synthetic oligo- nucleotides designed so as to yield the same nucleotide sequence as that reported for haFGF cDNA by Jaye et al with 2 exceptions. One (see FT) was designed to destroy the NcoI site spanning codon 67 and the other was designed so as to add HindIII and EcoRI cleavage sites following the TGA termination codon. Neither of these changes affects the amino acid sequence encoded. The synthetic gene is inserted into pAL12 and pAL13 making pAL12-haFGF and pAL13-haFGF respectively. It is part of a construct comprising: a first nucleotide sequence comprising an E. coli r3 promoter operably linked to a transcription initiation sequence; a second nucleotide sequence to terminate transcription; a third sequence comprising a ribosomal binding site and translation initiation codon operably linked to r3; a fourth sequence encoding a heterologous structural gene (eg AAN90994); a fifth sequence of an A-T rich oligomer; and a sixth sequence which is an

CC operator sequence to regulate expression of the fourth sequence. (Updated  
 CC on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 481 BP; 133 A; 118 C; 129 G; 101 T; 0 U; 0 Other;  
 Query Match 72.7%; Score 464; DB 1; Length 481;  
 Best Local Similarity 98.9%; Pred. No. 1.2e-133;  
 Matches 467; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 37 CCATGGCTGAAGGGAATCACCACCTTCACAGCCCTGACGAGAGTTTAACTGCTCC 96  
 DB 1 CCATGGCTGAAGGGAATCACCACCTTCACAGCCCTGACGAGAGTTTAACTGCTCC 60  
 QY 97 CAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCACTTCCTGAGGA 156  
 DB 61 CAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCACTTCCTGAGGA 120  
 QY 157 TCCTTCGGATGCGACAGTGGATGGAGCAGGAGGACGAGCCACGACCACTTCAGCTGC 216  
 DB 121 TCCTTCGGATGCGACAGTGGATGGAGCAGGAGGACGAGCCACGACCACTTCAGCTGC 180  
 QY 217 AGCTCAGTGGGAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACT 276  
 DB 181 AGCTCAGTGGGAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACT 240  
 QY 277 TGGCATGACACCGAGCGGCTTTTACGGCTCAGACACCAATGAGGAATGTTGT 336  
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 QY 337 TCCTTGAAGGCTGGAGGACCACTTACCACTATATATCAAGAGCATGACAGGA 396  
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 QY 397 AGAATGGTTTGGCTCAGAGAGATGGGAGCTGCAGCGGCTCTTAACTCACT 456  
 DB 361 AGAATGGTTTGGCTCAGAGAGATGGGAGCTGCAGCGGCTCTTAACTCACT 420  
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 ID ABV78179 standard; DNA; 468 BP.  
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 AC ABV78179;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Human DNA SEQ ID NO 63.  
 XX  
 KW RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;  
 KW virucide; protozoacide; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200255693-A2.  
 XX  
 PD 18-JUL-2002.  
 XX  
 PF 09-JAN-2002; 2002WO-EP000152.  
 XX  
 PR 09-JAN-2001; 2001DE-01000586.  
 PR 26-OCT-2001; 2001DE-01055280.  
 PR 29-NOV-2001; 2001DE-01058411.  
 PR 07-DEC-2001; 2001DE-01060151.  
 XX  
 PA (RIBO-) RIBOPHARMA AG.  
 XX  
 PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
 XX  
 DR WPI; 2002-590671/63.  
 XX  
 PT Inhibiting expression of target gene, useful e.g. for inhibiting  
 PT oncogenes, by administering double-stranded RNA complementary to the  
 PT target and having an overhang.  
 XX  
 PS Claim 10; Page 147; 203pp; German.

XX The invention relates to inhibiting expression of a target gene (I) in a  
 CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded  
 CC structure of at most 49 consecutive bases. At least part of one strand  
 CC (asi) of dsRNA is complementary to (I) and at least one end of dsRNA1  
 CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
 CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
 CC in humans, also genes in plasmodium or in viruses or viroids that are  
 CC pathogenic for humans, animals or plants. Introducing an overhang into  
 CC dsRNA greatly increases effectiveness for inhibiting gene expression,  
 CC both in vivo and in vitro and also increases stability and thus the  
 CC effective concentration inside the cell. The present sequence is that of  
 CC a gene related to the invention  
 XX  
 SQ Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;  
 Query Match 72.6%; Score 453.2; DB 6; Length 468;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-133;  
 Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 39 ATGGCTGAAGGGAAATCACCACCTTCACAGCCCTGACGAGAGTTTAACTGCTCCA 98  
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 QY 99 GGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCACTTCCTGAGGATC 158  
 DB 61 GGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCACTTCCTGAGGATC 120  
 QY 159 CTTCGGATGGCACAGTGGAGCAAGGGACAGAGCGACCCAGCACTTCAGCTGCAG 218  
 DB 121 CTTCGGATGGCACAGTGGAGCAAGGGACAGAGCGACCCAGCACTTCAGCTGCAG 180  
 QY 219 CTGAGTGGGAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTCTTG 278  
 DB 181 CTGAGTGGGAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTCTTG 240  
 QY 279 GCCATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATGAGGAATGTTGTTTC 338  
 DB 241 GCCATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATGAGGAATGTTGTTTC 300  
 QY 339 CTGGAAGGCTGGAGGAGCACTTACCACTATATATCAAGAGCATGACAGGAAG 398  
 DB 301 CTGGAAGGCTGGAGGAGCACTTACCACTATATATCAAGAGCATGACAGGAAG 360  
 QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAGCGGCTCTTAAACTCACTAT 458  
 DB 361 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAGCGGCTCTTAAACTCACTAT 420  
 QY 459 GGCGAAGCAATCTGTTCTCTCCCTCCAGTCTCTCTGATTAA 506  
 DB 421 GGCGAAGCAATCTGTTCTCTCCCTCCAGTCTCTCTGATTAA 468  
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 ID ABZ35755 standard; DNA; 468 BP.  
 XX  
 AC ABZ35755;  
 XX  
 DT 07-FEB-2003 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 63.  
 XX  
 KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;  
 KW protozoacide; gene expression; antisense; tumour; infection; Plasmodium;  
 KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;  
 KW Hepatitis C virus; human papilloma virus; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE10100588-A1.  
 XX  
 PD 18-JUL-2002.  
 XX  
 PF 09-JAN-2001; 2001DE-01000588.  
 XX  
 PR 09-JAN-2001; 2001DE-01000588.  
 XX  
 PA (RIBO-) RIBOPHARMA AG.

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Perfect score: 638
Sequence: 1 gaattcggggaacgggcacca.....ctggaattgtaagcaactt 638

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs. 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Query Match 72.6%; Score 463.2; DB 6; Length 468;

Best Local Similarity 99.4%; Pred. No. 2.2e-133;

Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

GenCore version 5.1.6

GenCore version 3.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 18:36:49 ; Search time 84 Seconds  
(without alignments)  
4214.984 Million cell updates/sec

**Title:** US-10-022-554A-3





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Db 181 TCAGCTGAGCTCAGTCCGGAAGCGTGGGAGGAGTGTATATAAGAGTACCGAGACTGG 240  
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Db 241 CCAGTACTTGGCCATGACACCGAGCGGCTTTTATAGCGCTCAGACACCAAAATGAGCA 300  
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Db 301 ATGTTTGTCTGGAAGGCTGGAGGAGCAACATTACACACTATATATCCAGAGCA 360  
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Db 421 GAATCATATGCGCAGGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTCATTAAG 480  
QY 509 AGATCTGTC 518  
Db 481 AGATCTGTC 490

RESULT 3

US-08-793-900-1  
; Sequence 1, Application US/08793900  
; Patent No. 6143518  
; GENERAL INFORMATION:  
; APPLICANT: CAMERON, Beatrice  
; APPLICANT: CROUZET, Joel  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: PROTEINS, PLASMIDS AND MODIFIED CELLS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, Mailstop 3043  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,900  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01178  
; FILING DATE: 14-SEP-1995  
; APPLICATION NUMBER: FR 94/11049  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky Esq., Martin F.  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: ST94069-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8501 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
US-08-793-900-1

Query Match 73.8%; Score 470.6; DB 3; Length 8501;  
Best Local Similarity 99.2%; Pred. No. 2.8e-140;  
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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QY 99 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAAGGGGGCCACTTCTCTGAGGATC 158  
Db 168 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAAGGGGGCCACTTCTCTGAGGATC 227  
QY 159 CTTCCGATGGGACAGTGGATGGGACAAAGGACAGGAGGACGACCAATTCAGCTGAG 218  
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QY 219 CTCAGTGGGAAAGCGTGGGAGGAGTGTATATAAGAGTACGAGACTGCGAGTACTTG 278  
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QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAAGCGGCTCTCGACTCAT 458  
Db 468 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAAGCGGCTCTCGACTCAT 527  
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Db 528 GCGCAGAAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGATTAAGAGATCTG 584

RESULT 4

US-09-929-945-3  
; Sequence 3, Application US/09929945  
; Patent No. 6642026  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-929-945-3

Query Match 72.6%; Score 463.2; DB 4; Length 468;  
Best Local Similarity 99.4%; Pred. No. 1.4e-138;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAAATACACACCTTTCAGAGCCCTGACGAGAGTAAATCTGCTTCA 98  
Db 1 ATGGCTGAAGGGGAAATACACACCTTTCAGAGCCCTGACGAGAGTAAATCTGCTTCA 60  
QY 99 GCGAATTACAAGAGCCCAAACTCTCTACTGTAGCAAGGGGGCCACTTCTCTGAGGATC 158  
Db 61 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAAGGGGGCCACTTCTCTGAGGATC 120  
QY 159 CTTCCGATGGGACAGTGGATGGGACAAAGGACAGGAGGACGACCAATTCAGCTGAG 218  
Db 121 CTTCCGATGGGACAGTGGATGGGACAAAGGACAGGAGGACGACCAATTCAGCTGAG 180  
QY 219 CTCAGTGGGAAAGCGTGGGAGGAGTGTATATAAGAGTACCGAGACTGCGCAGTACTTG 278  
Db 181 CTCAGTGGGAAAGCGTGGGAGGAGTGTATATAAGAGTACCGAGACTGCGCAGTACTTG 240

QY 279 GCATGGACGACGCGGCTTTTATACGGCTCAGACACCAATGAGAAATGTTGTTTC 338  
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Db 301 CTGAAAGGCTGGAGAGAACCAATTAACACCTATATATCCAAAGAGCATGAGAGAG 360  
QY 399 AATTGTTGTTGGCTCAAGAGAAATGGAGAGTCAAGCGGCTTAAACTCACTAT 458  
Db 361 AATTGTTGTTGGCTCAAGAGAAATGGAGAGTCAAGCGGCTTAAACTCACTAT 420  
QY 459 GGCCAGAAAGCAATCTGTTTCTCCCGCTCCAGCTCTCTCTGATTAA 506  
Db 421 GGCCAGAAAGCAATCTGTTTCTCCCGCTCCAGCTCTCTCTGATTAA 468

RESULT 5  
5175147-1  
; Patent No. 5175147  
; APPLICANT: FOLKMAN, MOSES J.; KATO, KOICHI  
; TITLE OF INVENTION: ACID-RESISTANT FGF COMPOSITION AND METHOD  
; OF TREATING ULCERATING DISEASES OF THE GASTROINTESTINAL TRACT  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/382,263  
; FILING DATE: 20-JUL-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 234,966  
; FILING DATE: 19-AUG-1988  
; SEQ ID NO:1:  
; LENGTH: 454  
5175147-1

Query Match 64.7%; Score 412.8; DB 6; Length 454;  
Best Local Similarity 96.1%; Pred. No. 1.9e-122;  
Matches 423; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 71 CTGACCGAGAGTAAATCTGCTCCAGGAAATTAACAGACCCCAACTCTCTACTG 130  
Db 4 CTTACTGGCAATGTTTAAATCTGCTCCAGGAAATTAACAGACCCCAACTCTCTACTG 63  
QY 131 TAGCAACGGGGCCACTTCTGAGGATCTTCCGGATGGACAGTGGAGCAAGGGA 190  
Db 64 CAGCAACGGGGCCACTTCTGAGGATCTTCCGGATGGACAGTGGAGCAAGGGA 123  
QY 191 CAGGAGCGACGACATTCAGCTCAGCTCAGTGGGAAAGCGTGGGGAGGTGTAT 250  
Db 184 AAAGAGTACCGAGCTGCCAGTCTTGGCAATGGACACCGGCTTTTATACGGCTC 243  
QY 311 ACAGACCAATGAGGAAATGTTTCTTGGAAAGGCTGGAGAGACCATTAACAC 370  
Db 244 ACAGACCAATGAGGAAATGTTTCTTGGAAAGGCTGGAGAGACCATTAACAC 303  
QY 371 CTATATATCAAGAGCATGAGAGAAATGGTTTGGCTCAAGAGAAATGGGAG 430  
Db 304 CTATATATCAAGAGCATGAGAGAAATGGTTTGGCTCAAGAGAAATGGGAG 363  
QY 431 CTGAAAGCGGCTTAAACTCACTATGCGCAAGGAAATGTTTCTCCCGCTGCC 490  
Db 364 CTGAAAGCGGCTTAAACTCACTATGCGCAAGGAAATGTTTCTCCCGCTGCC 423  
QY 491 AGTCTCTCTGATTAAAGAG 510  
Db 424 AGTCTCTCTGATTAAAG 443

RESULT 6  
5437995-1  
; Patent No. 5437995  
; APPLICANT: ICHIMORI, YUZO; KONDO, KOICHI; IGARASHI, KOICHI;  
; SENDO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AGAINST AN ACIDIC  
; FGF PROTEIN AND HYBRIDOMA FOR ITS PRODUCTION

; NUMBER OF SEQUENCES: 3  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/26,257  
; FILING DATE: 04-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 588,343  
; FILING DATE: 26-SEP-1990  
; SEQ ID NO:1:  
; LENGTH: 450  
5437995-1

Query Match 56.7%; Score 361.6; DB 6; Length 450;  
Best Local Similarity 94.8%; Pred. No. 4.9e-106;  
Matches 417; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

QY 71 CCTGACCGAGAGTAAATCTGCTCCAGGAAATTAACAGAGCCCAACTCTCTACTG 130  
Db 4 CTTACTCTGCAATGTTTAAATCTGCTCCAGGAAATTAACAGAGCCCAACTCTCTACTG 63  
QY 131 TAGCAACGGGGCCACTTCTGAGGATCTTCCGGATGGACAGTGGAGCAAGGGA 190  
Db 64 CAGCAACGGGGCCACTTCTGAGGATCTTCCGGATGGACAGTGGAGCAAGGGA 123  
QY 191 CAGGAGCGACGACATTCAGCTCAGCTCAGTGGGAAAGCGTGGGGAGGTGTAT 250  
Db 124 CAGGA-CGACGACGACATTCAGCTCAGTGGGAAAGCGTGGGGAGGTGTAT 182  
QY 251 AAAGAGTACCGAGCTGCCAGTCTTGGCAATGGACACCGGCTTTTATACGGCTC 310  
Db 183 AAAGAGTACCGAGCTGCCAGTCTTGGCAATGGACACCGGCTTTTATACGGCTC 241  
QY 311 ACAGACCAATGAGGAAATGTTTCTTGGAAAGGCTGGAGAGACCATTAACAC 370  
Db 242 ACAGACCAATGAGGAAATGTTTCTTGGAAAGGCTGGAGAGACCATTAACAC 301  
QY 371 CTATATATCAAGAGCATGAGAGAAATGGTTTGGCTCAAGAGAAATGGGAG 430  
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QY 431 CTGAAAGCGGCTTAAACTCACTATGCGCAAGGAAATGTTTCTCCCGCTGCC 490  
Db 361 CTGAAAGCGGCTTAAACTCACTATGCGCAAGGAAATGTTTCTCCCGCTGCC 419  
QY 491 AGTCTCTCTGATTAAAGAG 510  
Db 420 AGTCTCTCTGATTAAAG 439

RESULT 7  
US-09-030-613-14  
; Sequence 14, Application US/09030613  
; Patent No. 6083706  
; GENERAL INFORMATION:  
; APPLICANT: Floriewicz, Robert Z.  
; APPLICANT: Baird, J. Andrew  
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,613  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6083706tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.418C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900



Db 422 CTAGAAAGACTAGAGAAACCTTACACAGCTACATATCGAAAAACATCGAGAG 481  
Qy 399 AATTGGTTTGTGGCTCAAGAGATGGGAGCTGCAAAACGGGTCTCTAAATCACTAT 458  
Db 482 AACTGGTTGTAGGCTTAAAAAAATGGTCTCTGTAAGCTGGACACGAGCTCACTAT 541  
Qy 459 GCGCAGAAAGCAATCTGTTTCTCCCTCGCAGCTCTCTCTGATTAAAGA 509  
Db 542 GCGCAAAAGGCTATCTGTTCTGCTGCACTACCACTAGCTGCTCGACTAAGA 592

RESULT 10

US-09-929-945-6

: Sequence 6, Application US/09929945

: Patent No. 6642026

: GENERAL INFORMATION:

: APPLICANT: Stegmann, Thomas

: APPLICANT: Kordyum, Vitaliy A.

: APPLICANT: Chernykh, Svitlana I.

: APPLICANT: Slavchenko, Iryna Yu.

: APPLICANT: Vozianov, Olexandr

: TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT

: TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155

: FILE REFERENCE: CVGENG.008A

: CURRENT APPLICATION NUMBER: US/09/929,945

: NUMBER OF SEQ ID NOS: 8

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 6

: LENGTH: 630

: TYPE: DNA

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: Chemically synthesized sequence for human acidic

: OTHER INFORMATION: Fibroblast Growth Factor (140 amino acids) using

: OTHER INFORMATION: preferred codons for E. coli

: NAME/KEY: CDS

: LOCATION: (122)...(544)

US-09-929-945-6

Query Match 44.0%; Score 280.6; DB 4; Length 630;  
Best Local Similarity 78.2%; Pred. No. 5.4e-80;  
Matches 337; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 79 AGAGTTTATCTGCTCCAGGGAATACAGAGCCCAACCTCTCTACTGTAGCAAG 138  
Db 120 ATATGTTTAACTTCCGCGCGGAATTCMAAAACCCAAAGCTTCTTACTCGATTAACG 179  
Qy 139 GGGCCACTTCTGAGATCTCTCGGATGGCAGATGGATGGGAGGAGGAGGAGG 198  
Db 180 GAGCACACTTCTGCGAATCTGCGAGATGGCAGATGGGAGTGGGACTCGGCTCGC 239  
Qy 199 ACCAGCATTCAGCTCAGCTCAGTCCGGAAGGCTGGGAGGAGTGTATATAAGAGTA 258  
Db 240 ACCAGCATTCAGCTCAGCTCAGTCCGCGGAAGGCTGGGAGGAGTGTATATAAGTGA 299  
Qy 259 CCGAGACTGGCCAGTACTTGGCCATGAGCACCGAGCGGGCTTTTATAGGGTCAAGAC 318  
Db 300 CCGAGACTGGCCAGTACTTGGCCATGAGCACCGAGCGGGCTTCTGTATGGCTCAGACGC 359  
Qy 319 CAATGAGGAATGTTGTTCTCGAAGGCTGGAGAGAACATTAACACCTATATAT 378  
Db 360 CTACGAGAGATGTTTCTTCTAGAGAGCTAGAGAAACCAATTCACACGTACATAT 419  
Qy 379 CAAGAAGCATCGAGAGAAATGTTTGTGGCTCAAGAGAAATGGAGGCTCAAAAC 438  
Db 420 CGAAAAACATCGAGAGAACTGGTTGTAGGCTTAAAAAAATGGTCTCTTAAGC 479  
Qy 439 GGGTCTTAACTCACTATGCGCAAGAACATCTGTTCTCCCTCGCAGTCTCT 498  
Db 480 GTGGACACCGGACTCATATATGCGCAAGAGGCTATCTGTTCTGCGCACTACGAGT 539  
Qy 499 CTGATTAAAGA 509  
Db 540 CCGACTAAGA 550

RESULT 11

US-09-929-945-4  
: Sequence 4, Application US/09929945  
: Patent No. 6642026  
: GENERAL INFORMATION:  
: APPLICANT: Stegmann, Thomas  
: APPLICANT: Kordyum, Vitaliy A.  
: APPLICANT: Chernykh, Svitlana I.  
: APPLICANT: Slavchenko, Iryna Yu.  
: APPLICANT: Vozianov, Olexandr  
: TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
: TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
: FILE REFERENCE: CVGENG.008A  
: CURRENT APPLICATION NUMBER: US/09/929,945  
: CURRENT FILING DATE: 2001-08-15  
: NUMBER OF SEQ ID NOS: 8  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 4  
: LENGTH: 630  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: Chemically synthesized sequence for human acidic  
: OTHER INFORMATION: Fibroblast Growth Factor (134 amino acids) using  
: OTHER INFORMATION: preferred codons for E. coli  
: NAME/KEY: CDS  
: LOCATION: (122)...(526)  
US-09-929-945-4

Query Match 42.0%; Score 268.2; DB 4; Length 630;  
Best Local Similarity 78.5%; Pred. No. 5.1e-76;  
Matches 321; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 101 GAATTACAGAGCCCAACCTCTCTACTGTAGCAAGGGGGCCACTCTCTGAGGATCCT 160  
Db 124 GAATTACAAAAACCCAAAGCTTCTTACTGCTAGTACGAGAGCACTTCTGGAATTC 183  
Qy 161 TCCGATGGCAGATGGATGGCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 220  
Db 184 GCGAGATGGCAGATGGATGGGACTCGGATCGCTCCGACGACATTCAGCTCAACT 243  
Qy 221 CAGTCCGGAAGGCTGGGAGGCTGTATATAAGAGTACGAGACTGCGCAGTCTGCGC 280  
Db 244 CTGCGCGGAAGGCTGGGAGGCTGTATATAAGTACGAGGAGTGGCCAGTCTGCGC 303  
Qy 281 CATGACACCGGCGCTTTTATAGGCTCAGACACCAATAGAGGAATGTTGTTCT 340  
Db 304 CATGACACCGGCTTCTGTATGCTCAGACAGCGCTTACGAGGAATGTTGTTCT 363  
Qy 341 GGAAGGCTGGGAGAGAACCTTACACACTTATATCCAGAGAGCATCGAGAGAGAA 400  
Db 364 AGAAGACTAGAGAAACCAATTCACACGTACATATCGAAAAACATCGAGAGAA 423  
Qy 401 TTGGTTTGGCTCAAGAGAAATGGGAGCTGCAAAACGGGTCTCTTAAAACTCCTATGG 460  
Db 424 CTGGTTTGGAGCTTAAAAAAATGGTCTCTTAAGCGTGACCAACGAGCTCCTATGG 483  
Qy 461 CCGAAGCAATCTGTTCTTCTCCCTGCGAGTCTCTCTGATTAAAGA 509  
Db 484 CCAAGGCTATCTGTTCTGCGCACTACCAAGTGGAGTCTCGACTAAGA 532

RESULT 12

5514566-3

: Patent No. 5514566

: APPLICANT: FIDES, JOHN C.; ABRAHAM, JUDITH A.

: TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT

: FIBROBLAST GROWTH FACTORS

: NUMBER OF SEQUENCES: 21

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/417,022

: FILING DATE: 05-APR-1995

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 809,163

: FILING DATE: 16-DEC-1985

: APPLICATION NUMBER: 775,521

: FILING DATE: 12-SEP-1985

: SEQ ID NO:3:

: LENGTH: 197

5514566-3

Query Match 27.4%; Score 174.8; DB 6; Length 197;  
Best Local Similarity 98.9%; Pred. No. 2.3e-46;  
Matches 176; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 36 GCGATGGCTGAAGCGGAATCCACCTTCCAGCCCTGACCGAGAGTTTAACTTCGCT 95  
DB |||||||  
7 GCGATGGCTGAAGCGGAATCCACCTTCCAGCCCTGACCGAGAGTTTAACTTCGCT 66  
DB |||||||

QY 96 CAGGGAATACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCTGAGG 155  
DB |||||||

QY 67 CAGGGAATACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCTGAGG 126  
DB |||||||

QY 156 ATCTTCCGATGGCAGCTGGATGGGCAAGGAGCAGAGGCGACACAGCACTTACG 213  
DB |||||||

QY 127 ATCTTCCGATGGCAGCTGGATGGGCAAGGAGCAGAGGCGACACAGCACTTACG 184  
DB |||||||

RESULT 13  
US-08-070-165F-1  
; Sequence 1, Application US/08070165F  
; Patent No. 5750365  
; GENERAL INFORMATION:  
; APPLICANT: Chiu, Ing-Ming  
; APPLICANT: Poulin, Matthew L  
; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ing-Ming Chiu  
; STREET: S2052 Davis Medical Research Center, 480 West  
; STREET: 9th Avenue  
; CITY: Columbus  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 43210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/070.165F  
; CLASSIFICATION: 435  
; TELEPHONE: (614)-293-8093  
; TELEFAX: (614)-293-5631  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: No. 5750365ophthalmus viridescens  
; DEVELOPMENTAL STAGE: Adult  
; TISSUE TYPE: Brain  
; IMMEDIATE SOURCE:  
; CLONE: MP 75-1  
; POSITION IN GENOME:  
; UNITS: bp  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..261  
; PUBLICATION INFORMATION:  
; AUTHORS: Patrie, Kevin M  
; AUTHORS: Botelho, Mary Jane  
; AUTHORS: Ray, Subir K  
; AUTHORS: Mehta, Veela B  
; AUTHORS: Chiu, Ing-Ming  
; JOURNAL: J. Biol. Chem.  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 261

Query Match 25.9%; Score 165; DB 1; Length 261;  
Best Local Similarity 77.0%; Pred. No. 3.8e-43;

Matches 201; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 90 CTGCTCCAGGAAATACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTC 149  
DB |||||||

DB 1 CTTCCCAATGGAATACTACAGAGCCCTTAAGCTCTCTACTGTAGCAACGGAGGTACTTC 60  
QY 150 CTAGCATCTCTCCGATGGCAGCTGGATGGGCAAGGAGCAGAGGCGACGACACATT 209  
DB |||||||

DB 61 CTGCGAATCTCCAGATGGCAGCTGGATGGGCAAGGAGCAGAGGCGACGACACATT 120  
QY 210 CAGTCTGAGCTCAGTCCGGAAGAGCTGGGGGAGGTCTATATAAGAGATACCGAGACTGGC 269  
DB |||||||

DB 121 CAGTCTGAGCTCAGTCCGGAAGAGCTGGGGGAGGTCTATATAAGAGATACCGAGACTGGC 180  
QY 270 CAGTCTGAGCTCAGTCCGGAAGAGCTGGGGGAGGTCTATATAAGAGATACCGAGACTGGC 329  
DB |||||||

DB 181 CAGTCTGAGCTCAGTCCGGAAGAGCTGGGGGAGGTCTATATAAGAGATACCGAGACTGGC 240  
QY 330 TGTCTGCTTCTGGAAAGCTG 350  
DB |||||||

DB 241 TGCCTGTTCTTGGAGCGACTG 261

RESULT 14  
US-08-885-418-1  
; Sequence 1, Application US/08885418  
; Patent No. 5925528  
; GENERAL INFORMATION:  
; APPLICANT: Chiu, Ing-Ming  
; APPLICANT: Poulin, Matthew L  
; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ing-Ming Chiu  
; STREET: S2052 Davis Medical Research Center, 480 West  
; STREET: 9th Avenue  
; CITY: Columbus  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 43210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/885.418  
; CLASSIFICATION: 435  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (614)-293-8093  
; TELEFAX: (614)-293-5631  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: No. 5925528ophthalmus viridescens  
; DEVELOPMENTAL STAGE: Adult  
; TISSUE TYPE: Brain  
; IMMEDIATE SOURCE:  
; CLONE: MP 75-1  
; POSITION IN GENOME:  
; UNITS: bp  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..261  
; PUBLICATION INFORMATION:  
; AUTHORS: Patrie, Kevin M  
; AUTHORS: Botelho, Mary Jane  
; AUTHORS: Ray, Subir K  
; AUTHORS: Mehta, Veela B  
; AUTHORS: Chiu, Ing-Ming  
; JOURNAL: J. Biol. Chem.



30 120.8 18.9 432 15 US-10-168-050-6 Sequence 6, Appli  
31 120.6 18.9 3877 15 US-10-131-985-6 Sequence 6, Appli  
32 120.6 18.9 6514 14 US-10-090-983-1 Sequence 1, Appli  
33 119.8 18.8 1374 10 US-09-775-964-26 Sequence 26, Appl  
34 119.8 18.8 16602 15 US-10-311-455-700 Sequence 700, App  
35 119.8 18.8 18357 17 US-10-433-793-114 Sequence 114, App  
36 119.2 18.7 441 9 US-09-802-365-3 Sequence 3, Appli  
37 119.2 18.7 441 9 US-09-886-856-3 Sequence 11, Appl  
38 119.2 18.7 444 15 US-10-155-785-11 Sequence 7, Appli  
39 119.2 18.7 474 9 US-09-802-365-7 Sequence 7, Appli  
40 119.2 18.7 474 9 US-09-886-856-7 Sequence 7, Appli  
41 119.2 18.7 489 9 US-09-934-706-11 Sequence 11, Appl  
42 119.2 18.7 489 13 US-10-344-634-7 Sequence 7, Appli  
43 119.2 18.7 630 16 US-10-408-415-4 Sequence 4, Appli  
44 119.2 18.7 1182 13 US-10-344-634-13 Sequence 13, Appl  
45 119.2 18.7 1527 9 US-09-934-706-15 Sequence 15, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-044-090-225  
; Sequence 225, Application US/10044090  
; Publication No. US20020137081A1  
; GENERAL INFORMATION:  
; APPLICANT: Olga Bandman  
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
; FILE REFERENCE: PA-0028 US  
; CURRENT APPLICATION NUMBER: US/10/044,090  
; CURRENT FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PERL Program  
; SEQ ID NO 225  
; LENGTH: 4087  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20020137081A1 336376.2  
US-10-044-090-225

Query Match 94.3%; Score 601.8; DB 14; Length 4087;  
Best Local Similarity 98.6%; Pred. No. 3.8e-192;  
Matches 628; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAAGCGGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATCACCACC 62  
DB 470 AGTCTTGAAGAGCGGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATCACCACC 529  
QY 63 TTACAGCCCTCAGCAGAGAGTTTAATCTGCTCCAGGAGATTTACAGAGCCCAAACTC 122  
DB 530 TTACAGCCCTCAGCAGAGAGTTTAATCTGCTCCAGGAGATTTACAGAGCCCAAACTC 589  
QY 123 CTCTACTGTAGCAACGGGGGCCCACTCTCTGAGGATCTTCGGATGGCAGCTGGATGGG 182  
DB 590 CTCTACTGTAGCAACGGGGGCCCACTCTCTGAGGATCTTCGGATGGCAGCTGGATGGG 649  
QY 183 ACAAGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 242  
DB 650 ACAAGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 709  
QY 243 GTGTATATAAGAGTACCGAGCTGCGCAGTACTTGGCCATGGACACCGAGCGCTTTTA 302  
DB 710 GTGTATATAAGAGTACCGAGCTGCGCAGTACTTGGCCATGGACACCGAGCGCTTTTA 769  
QY 303 TACGGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 362  
DB 770 TACGGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 829  
QY 363 TACAACACCTATATATCAAGAGCAGTGCAGAGAGATTTGGTTTGTGGCTTCAGAGAG 422  
DB 830 TACAACACCTATATATCAAGAGCAGTGCAGAGAGATTTGGTTTGTGGCTTCAGAGAG 889  
QY 423 AATGGGAGCTCAAAAGCGGCTCTAAACTCCTATGGCCAGAGAGCAATCTTTTTC 482  
DB 890 AATGGGAGCTCAAAAGCGGCTCTAAACTCCTATGGCCAGAGAGCAATCTTTTTC 949  
QY 483 CCCCTGCCAGTCTCTCTGATTAAAGAGATCTGTCTT-GGTGTGACCACTCCAGAGAG 541

DB 950 CCCCTGCCAGTCTCTCTGATTAAAGAGATCTGTGTGGGTGTGACCACTCCAGAGAG 1009  
QY 542 TTTCAGAGGGGTCTCACTGCTGAGCCCAAAATGTTCCCTTGACCAATTTGGCTGCTA 601  
DB 1010 TTTCAGAGGGGTCTCACTGCTGAGCCCAAAATGTTCCCTTGACCAATTTGGCTGCTA 1068  
QY 602 ACCCCCAAGCGGCCCAAGCAGCAGCTGATTTGTAAGCAACTT 638  
DB 1069 ACCCCCAAGCGGCCCAAGCAGCAGCTGATTTGTAAGCAACTT 1105

#### RESULT 2

US-09-902-460-3  
; Sequence 3, Application US/09902460  
; Publication No. US20030040042A1  
; GENERAL INFORMATION:  
; APPLICANT: FIDDES, J.C.  
; ABRHAM, J.D.  
; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH  
; FACTOR ANALOG  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FORSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/902,460  
; FILING DATE: 09-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/098,628  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 21900-20089.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 638 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 91...555  
; OTHER INFORMATION:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-902-460-3

Query Match 86.2%; Score 549.8; DB 10; Length 638;  
Best Local Similarity 98.5%; Pred. No. 6e-175;  
Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAAGCGGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATCACCACC 62  
DB 55 AGTCTTGAAGAGCGGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATCACCACC 114  
QY 63 TTACAGCCCTCAGCAGAGAGTTTAATCTGCTCCAGGAGATTTACAGAGCCCAAACTC 122  
DB 115 TTACAGCCCTCAGCAGAGAGTTTAATCTGCTCCAGGAGATTTACAGAGCCCAAACTC 174  
QY 123 CTCTACTGTAGCAACGGGGGCCCACTCTCTGAGGATCTTCGGATGGCAGCTGGATGGG 182  
DB 175 CTCTACTGTAGCAACGGGGGCCCACTCTCTGAGGATCTTCGGATGGCAGCTGGATGGG 234



QY 183 ACAAGGACAGAGGACGACGACATTCAGCTGAGCTCAGTGGGAAAGCGTGGGGAG 242  
 Db 235 ACAAGGACAGAGGACGACGACATTCAGCTGAGCTCAGTGGGAAAGCGTGGGGAG 294  
 QY 243 GTCTATATAAGAGTACGAGAGTGGCCAGTCTTGGCCATGAGACACGAGCGGCTTTTA 302  
 Db 295 GTGTATATAAGAGTACGAGAGTGGCCAGTCTTGGCCATGAGACACGAGCGGCTTTTA 354  
 QY 303 TAGGCTCACAGACACCAATAGGAATGTTTCTTCTGAAAGGCTGGAGGAGAACAT 362  
 Db 355 TAGGCTCACAGACACCAATAGGAATGTTTCTTCTGAAAGGCTGGAGGAGAACAT 414  
 QY 363 TACACACCTATATATCCAGAGAGCATCCAGAGAGAGATGTTTGGCTCAGAGAG 422  
 Db 415 TACACACCTATATATCCAGAGAGCATCCAGAGAGAGATGTTTGGCTCAGAGAG 474  
 QY 423 AATGGAGCTGCAAGCGGCTCTTAAACTCATTATGCGCAGAGAGCAATCTTGTCTC 482  
 Db 475 AATGGAGCTGCAAGCGGCTCTTAAACTCATTATGCGCAGAGAGCAATCTTGTCTC 534  
 QY 483 CCCTGCGAGCTCTCTGATTAAGAGATCTGTTCT-GGTGTGACCATCCAGAGAG 541  
 Db 535 CCCTGCGAGCTCTCTGATTAAGAGATCTGTTCTGCGGTGTGACCATCCAGAGAG 594  
 QY 542 TTTCAGGCGGCTCTCACTGTTGACCCCAAAATGTTCCCTTGA 586  
 Db 595 TTTCAGGCGGCTCTCACTGTTGACCCCAAAATGTTCCCTTGA 638  
 RESULT 3  
 US-10-388-410-8  
 ; Sequence 8, Application US/10388410  
 ; Publication No. US20030157548A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAWA, HIROYUKI  
 ; APPLICANT: TAKAHASHI, HITOSHI  
 ; APPLICANT: TRITANI, SHUJI  
 ; TITLE OF INVENTION: METHOD FOR DIAGNOSING SCHIZOPHRENIA USING OBJECTIVE INDICES  
 ; FILE REFERENCE: 235447USOCONT  
 ; CURRENT APPLICATION NUMBER: US/10/388.410  
 ; FILING DATE: 2003-03-17  
 ; PRIOR FILING DATE: 2003-03-17  
 ; PRIOR FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: JP 2000-061775  
 ; PRIOR FILING DATE: 2000-03-07  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 490  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-388-410-8  
 Query Match 76.1%; Score 485.2; DB 15; Length 490;  
 Best Local Similarity 99.4%; Pred. No. 3.7e-153;  
 Matches 487; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 29 CTGCTGAGCCATGCTGAGAGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAA 88  
 Db 1 CTGCTGAGCCATGCTGAGAGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAA 60  
 QY 89 TCTGCTCCAGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAAGCGGCGCACTT 148  
 Db 61 TCTGCTCCAGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAAGCGGCGCACTT 120  
 QY 149 CTTGAGATCTCTCCGATGGCAGTGGATGGGACAGAGGACAGGAGCGACACAT 208  
 Db 121 CTTGAGATCTCTCCGATGGCAGTGGATGGGACAGAGGACAGGAGCGACACAT 180  
 QY 209 TGAGCTGAGCTCTCCGATGGCAGTGGATGGGAGGTTATATAAGAGTACCGAGATCG 268  
 Db 181 TGAGCTGAGCTCTCCGATGGCAGTGGATGGGAGGTTATATAAGAGTACCGAGATCG 240  
 QY 269 CAGTACTTGGCATGACACCTCCGAGGCTTTTATACGGCTCAGACACCAATAGAGA 328  
 Db 241 CAGTACTTGGCATGACACCTCCGAGGCTTTTATACGGCTCAGACACCAATAGAGA 300  
 QY 329 ATGTTTGTCTCGAAGGCTGAGGAGAACCAATTACACACCTTATATATCCAGAGAGCA 388  
 Db 329 ATGTTTGTCTCGAAGGCTGAGGAGAACCAATTACACACCTTATATATCCAGAGAGCA 388

Db 301 ATGTTTGTCTCGAAGGCTGAGGAGAACCAATTACACACCTTATATATCCAGAGAGCA 360  
 QY 389 TCCAGAGAGAAATGTTTGTGCTTCAAGAGAAATGGAGCTGCAAAACGCGTCTTAA 448  
 Db 361 TCCAGAGAGAAATGTTTGTGCTTCAAGAGAAATGGAGCTGCAAAACGCGTCTTAA 420  
 QY 449 AACTCACTATGCGCAGAGCAATCTTGTCTTCCCGCTGCGAGTCTCTCTGATTAAAG 508  
 Db 421 GACTCACTATGCGCAGAGCAATCTTGTCTTCCCGCTGCGAGTCTCTCTGATTAAAG 480  
 QY 509 AGATCTGTTT 518  
 Db 481 AGATCTGTTT 490  
 RESULT 4  
 US-10-641-643-1390  
 ; Sequence 1390, Application US/10641643  
 ; Publication No. US20040077003A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
 ; GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/641.643  
 ; FILING DATE: 14-Aug-2003  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: <Unknown>  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1390:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 490 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: g396163  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1390 :  
 US-10-641-643-1390  
 Query Match 76.1%; Score 485.2; DB 17; Length 490;  
 Best Local Similarity 99.4%; Pred. No. 3.7e-153;  
 Matches 487; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 29 CTGCTGAGCCATGCTGAGAGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAA 88  
 Db 1 CTGCTGAGCCATGCTGAGAGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAA 60  
 QY 89 TCTGCTCCAGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAAGCGGCGCACTT 148  
 Db 61 TCTGCTCCAGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAAGCGGCGCACTT 120  
 QY 149 CTTGAGATCTCTCCGATGGCAGTGGATGGGACAGAGGACAGGAGCGACACAT 208  
 Db 121 CTTGAGATCTCTCCGATGGCAGTGGATGGGACAGAGGACAGGAGCGACACAT 180

QY 209 TCAGCTGCAGCTCAGTGGCGAAGCGTGGGGAGGTGTATATAAGATGACCGAGCTGG 268  
Db 181 TCAGCTGCAGCTCAGTGGCGAAGCGTGGGGAGGTGTATATAAGATGACCGAGCTGG 240  
QY 269 CCAGTACTTGGCCATGACACCGGCGCTTTATACGGCTCAGACACCAATGAGGA 328  
Db 241 CCAGTACTTGGCCATGACACCGGCGCTTTATACGGCTCAGACACCAATGAGGA 300  
QY 329 ATGTTTGTTCCTGGAAAGCGCTGGAGGAGAACATTAACACACCTATATATCAAGAAGCA 388  
Db 301 ATGTTTGTTCCTGGAAAGCGCTGGAGGAGAACATTAACACACCTATATATCAAGAAGCA 360  
QY 389 TGCAGAGAAGATGTTGTTGCTGGCTCAAGAGATGGAGCTGCAACCGCGTCTTAA 448  
Db 361 TGCAGAGAAGATGTTGTTGCTGGCTCAAGAGATGGAGCTGCAACCGCGTCTTAA 420  
QY 449 AACTACTATGGCCGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGANTAAAG 508  
Db 421 GACTACTATGGCCGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGANTAAAG 480  
QY 509 AGATCTGTTT 518  
Db 481 AGATCTGTTT 490

#### RESULT 5

US-09-929-918-3  
; Sequence 3, Application US/09929918  
; Patent No. US20020090678A1  
; GENERAL INFORMATION:

; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF  
; FILE REFERENCE: PHAGE 006A  
; CURRENT APPLICATION NUMBER: US/09/929,918  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-929-918-3

Query Match 72.6%; Score 463.2; DB 9; Length 468;  
Best Local Similarity 99.4%; Pred. No. 1e-145;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 ATGCTGTAAGGGGAATCAACCTTCTACTGTAGACGCGGCGCACTTCTCGAGATC 98  
Db 1 ATGCTGTAAGGGGAATCAACCTTCTACTGTAGACGCGGCGCACTTCTCGAGATC 60  
QY 99 GGGGAATTACAGAGCCCAATCTCTCTACTGTAGACGCGGCGCACTTCTCGAGATC 158  
Db 61 GGGGAATTACAGAGCCCAATCTCTCTACTGTAGACGCGGCGCACTTCTCGAGATC 120  
QY 159 CTTCGGATGCGACGAGTGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTCTG 218  
Db 121 CTTCGGATGCGACGAGTGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTCTG 180  
QY 219 CTAGTGGGAAGCGTGGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTCTG 278  
Db 181 CTAGTGGGAAGCGTGGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTCTG 240  
QY 279 GCATGACACCGACGCGGCTTTTATACGCTCAGACACCAATGAGGATGTTGTTTC 338  
Db 241 GCATGACACCGACGCGGCTTTTATACGCTCAGACACCAATGAGGATGTTGTTTC 300  
QY 339 CTGGAAGGCTGGAGGAGAACATTAACACCTATATATCAAGAAGCATGAGAGAG 398  
Db 301 CTGGAAGGCTGGAGGAGAACATTAACACCTATATATCAAGAAGCATGAGAGAG 360  
QY 399 AATTGTTTGTGGCTCAAGAGATGGAGCTGCAGGCGCTTCTTAARACTACTAT 458  
Db 361 AATTGTTTGTGGCTCAAGAGATGGAGCTGCAGGCGCTTCTTAARACTACTAT 420  
QY 459 GGCAGAGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGANTAA 506  
Db 421 GGCAGAGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGANTAA 468

#### RESULT 7

US-10-280-864-3  
; Sequence 3, Application US/10280864  
; Publication No. US20030054492A1  
; GENERAL INFORMATION:

; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT

Db 361 AATTGTTTGTGGCTTCAAGAGATGGAGCTGCAAGCGGCTTCTCGACTACTAT 420  
QY 459 GGCAGAGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGANTAA 506  
Db 421 GGCAGAGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGANTAA 468

#### RESULT 6

US-09-929-945-3  
; Sequence 3, Application US/09929945  
; Patent No. US2002015532A1  
; GENERAL INFORMATION:

; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: FIBROBLAST GROWTH FACTOR 155  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-929-945-3

Query Match 72.6%; Score 463.2; DB 9; Length 468;  
Best Local Similarity 99.4%; Pred. No. 1e-145;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 ATGCTGTAAGGGGAATCAACCTTCTACTGTAGACGCGGCGCACTTCTCGAGATC 98  
Db 1 ATGCTGTAAGGGGAATCAACCTTCTACTGTAGACGCGGCGCACTTCTCGAGATC 60  
QY 99 GGGGAATTACAGAGCCCAATCTCTCTACTGTAGACGCGGCGCACTTCTCGAGATC 158  
Db 61 GGGGAATTACAGAGCCCAATCTCTCTACTGTAGACGCGGCGCACTTCTCGAGATC 120  
QY 159 CTTCGGATGCGACGAGTGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTCTG 218  
Db 121 CTTCGGATGCGACGAGTGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTCTG 180  
QY 219 CTAGTGGGAAGCGTGGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTCTG 278  
Db 181 CTAGTGGGAAGCGTGGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTCTG 240  
QY 279 GCATGACACCGACGCGGCTTTTATACGCTCAGACACCAATGAGGATGTTGTTTC 338  
Db 241 GCATGACACCGACGCGGCTTTTATACGCTCAGACACCAATGAGGATGTTGTTTC 300  
QY 339 CTGGAAGGCTGGAGGAGAACATTAACACCTATATATCAAGAAGCATGAGAGAG 398  
Db 301 CTGGAAGGCTGGAGGAGAACATTAACACCTATATATCAAGAAGCATGAGAGAG 360  
QY 399 AATTGTTTGTGGCTCAAGAGATGGAGCTGCAGGCGCTTCTTAARACTACTAT 458  
Db 361 AATTGTTTGTGGCTCAAGAGATGGAGCTGCAGGCGCTTCTTAARACTACTAT 420  
QY 459 GGCAGAGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGANTAA 506  
Db 421 GGCAGAGAAGCAATCTGTTTCTCCCTGCCAGTCTCTCTGANTAA 468

; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/10/280,864  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: US/09/929,945  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-280-864-3

Query Match 72.6%; Score 463.2; DB 15; Length 468;  
Best Local Similarity 99.4%; Pred. No. 1e-145;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAAAGTTTAACTTGCCTCCA 98  
Db 1 ATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAAAGTTTAACTTGCCTCCA 60  
QY 99 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGCGGCGGCTCTCTCTGAGGATC 158  
Db 61 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGCGGCGGCTCTCTCTGAGGATC 120  
QY 159 CTTCCGGATGGCAGACAGTGGATGGGACAGGAGGACAGGAGGACACGACCAATTCAGCTGCAG 218  
Db 121 CTTCCGGATGGCAGACAGTGGATGGGACAGGAGGACAGGAGGACACGACCAATTCAGCTGCAG 180  
QY 219 CTCAGTGGGAAAGCCTGCGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTG 278  
Db 181 CTCAGTGGGAAAGCCTGCGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTG 240  
QY 279 GCATGGACACCGACCGGCTTTTATACGGCTTCACAGACCAAAATGAGAAATGTTTGTTC 338  
Db 241 GCATGGACACCGACCGGCTTTTATACGGCTTCACAGACCAAAATGAGAAATGTTTGTTC 300  
QY 339 CTGGAAGGCTGGAGAGAACCAATTACCAACCTATATATCAAGAGCATGCGAGAG 398  
Db 301 CTGGAAGGCTGGAGAGAACCAATTACCAACCTATATATCAAGAGCATGCGAGAG 360  
QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGAGCTGCAAAAGCGGCTCTTAACTACTAT 458  
Db 361 AATTGGTTTGTGGCTCAAGAGAAATGGAGCTGCAAAAGCGGCTCTTAACTACTAT 420  
QY 459 GGCAGAAAGCAATCTTCTTCCCTGCGAGTCTCTCTGATTA 506  
Db 421 GGCAGAAAGCAATCTTCTTCCCTGCGAGTCTCTCTGATTA 468

RESULT 8

US-10-649-480-3  
; Sequence 3, Application US/10649480  
; Publication No. US20040115769A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/10/649,480  
; CURRENT FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: 10/649,480  
; PRIOR FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-649-480-3

Query Match 72.6%; Score 463.2; DB 17; Length 468;  
Best Local Similarity 99.4%; Pred. No. 1e-145;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAAAGTTTAACTTGCCTCCA 98  
Db 1 ATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAAAGTTTAACTTGCCTCCA 60  
QY 99 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGCGGCGGCTCTCTCTGAGGATC 158  
Db 61 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGCGGCGGCTCTCTCTGAGGATC 120  
QY 159 CTTCCGGATGGCAGACAGTGGATGGGACAGGAGGACAGGAGGACACGACCAATTCAGCTGCAG 218  
Db 121 CTTCCGGATGGCAGACAGTGGATGGGACAGGAGGACAGGAGGACACGACCAATTCAGCTGCAG 180  
QY 219 CTCAGTGGGAAAGCCTGCGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTG 278  
Db 181 CTCAGTGGGAAAGCCTGCGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTG 240  
QY 279 GCATGGACACCGACCGGCTTTTATACGGCTTCACAGACCAAAATGAGAAATGTTTGTTC 338  
Db 241 GCATGGACACCGACCGGCTTTTATACGGCTTCACAGACCAAAATGAGAAATGTTTGTTC 300  
QY 339 CTGGAAGGCTGGAGAGAACCAATTACCAACCTATATATCAAGAGCATGCGAGAG 398  
Db 301 CTGGAAGGCTGGAGAGAACCAATTACCAACCTATATATCAAGAGCATGCGAGAG 360  
QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGAGCTGCAAAAGCGGCTCTTAACTACTAT 458  
Db 361 AATTGGTTTGTGGCTCAAGAGAAATGGAGCTGCAAAAGCGGCTCTTAACTACTAT 420  
QY 459 GGCAGAAAGCAATCTTCTTCCCTGCGAGTCTCTCTGATTA 506  
Db 421 GGCAGAAAGCAATCTTCTTCCCTGCGAGTCTCTCTGATTA 468

RESULT 9

US-09-929-918-1  
; Sequence 1, Application US/09929918  
; Patent No. US2002090678A1  
; GENERAL INFORMATION:  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: PHASE-DEPENDENT SUPER PRODUCTION OF  
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES  
; FILE REFERENCE: PHAGE.006A  
; CURRENT APPLICATION NUMBER: US/09/929,918  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/318,288  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: This sequence was chemically synthesized based  
; OTHER INFORMATION: upon the amino acid sequence of human acidic  
; OTHER INFORMATION: fibroblast growth factor (155 amino acids) using  
; OTHER INFORMATION: codons which are used in highly expressed proteins from E. coli.  
; NAME/KEY: CDS  
; LOCATION: (122)....(590)  
US-09-929-918-1

Query Match 49.2%; Score 314.2; DB 9; Length 630;  
Best Local Similarity 79.2%; Pred. No. 2.9e-95;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAAAGTTTAACTTGCCTCCA 98  
Db 122 ATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTTACCGGTTAAACGAGAAATTAACCTTCGCCC 181  
QY 99 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGCGGCGGCTCTCTCTGAGGATC 158  
Db 182 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGCGGCGGCTCTCTCTGAGGATC 241  
QY 159 CTTCCGGATGGCAGACAGTGGATGGGACAGGAGGACAGGAGGACACGACCAATTCAGCTGCAG 218

Db 242 CTGCGAGTGGGACAGTACATGGGAGCTGCGGATCGCTCCGACGACACATTCAGCTGCAA 301  
QY 219 CTCAGTGGCGAAAGCGTGGGGAGGTGTATATAAAGATGACGAGACTGGCCAGTACTTG 278  
Db 302 CTCTCGCGCGAAAGCGTGGAGAGGTCTATATCAAGTGCAGCGAGACTGGCCAGTACTT 361  
QY 279 GCGATGACACCGGCGGTCTTTACGGCTTCACAGACACCAAAATGAGAAATGTTGTTTC 338  
Db 362 GCGATGACACCGGCGGTCTTTATGATGGCTTCACAGAGCGCTTACGAGAAATGCTGTTT 421  
QY 339 CTGAAAGGCTGGAGGAGAACCTTACAAACCTTATATCCAGAGCATGACAGAGAG 398  
Db 422 CTGAAAGGCTAGAGAAACCTTACAAACCTTATATCCAGAGCATGACAGAGAG 481  
QY 399 AATTGCTTTGCTGCTCAGAGAGTGGAGCTGCAAAAGCGGTCTTAAACTCACTAT 458  
Db 482 AACTGCTTTGAGGCTTTAAAAAAATGTTCTGTAAGCGTGGACCAAGCTCACTAT 541  
QY 459 GCGCAAGAACCAATCTTTGTTTCTCCCTCCGAGTCTCTCTGATTAAAGA 509  
Db 542 GCGCAAGAACCAATCTTTGTTTCTCCCTCCGAGTCTCTGATTAAAGA 592

RESULT 10

US-09-929-945-1

; Sequence 1, Application US/09929945  
; Patent No. US2002015532A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svetlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozlanov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized sequence for human acidic  
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
; NAME/KEY: CDS  
; LOCATION: (122)...(590)  
US-09-929-945-1

Query Match 49.2%; Score 314.2; DB 9; Length 630;  
Best Local Similarity 79.2%; Pred. No. 2.9e-95;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
QY 39 ATGCTGAAGGGGAAATACCACTTTCAGAGCTGACGAGAGTGTAACTTCCCTCCA 98  
Db 122 ATGCTGAAGGGGAAATACCACTTTCAGAGCTGACGAGAGTGTAACTTCCCTCCA 181  
QY 99 GCGAATTACAAAGAGCCCAAACTCTTCTAGTACGAGAGTGTAACTTCCCTCCA 158  
Db 182 GCGAATTACAAAGAGCCCAAACTCTTCTAGTACGAGAGTGTAACTTCCCTCCA 241  
QY 159 CTTCGGATGGCAGTGGATGGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
Db 242 CTGCGAGTGGCAGTGGATGGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 301  
QY 219 CTCAGTGGCGAAAGCGTGGGGAGGTGTATAAAGATGACGAGACTGGCCAGTACTTG 278  
Db 302 CTCTCGCGCGAAAGCGTGGAGAGGTCTATATCAAGTGCAGCGAGACTGGCCAGTACTT 361  
QY 279 GCGATGACACCGGCGGTCTTTACGGCTTCACAGACACCAAAATGAGAAATGTTGTTTC 338  
Db 362 GCGATGACACCGGCGGTCTTTATGATGGCTTCACAGAGCGCTTACGAGAAATGCTGTTT 421  
QY 339 CTGAAAGGCTGGAGGAGAACCTTACAAACCTTATATCCAGAGCATGACAGAGAG 398  
Db 422 CTGAAAGGCTAGAGAAACCTTACAAACCTTATATCCAGAGCATGACAGAGAG 481  
QY 399 AATTGCTTTGCTGCTCAGAGAGTGGAGCTGCAAAAGCGGTCTTAAACTCACTAT 458  
Db 482 AACTGCTTTGAGGCTTTAAAAAAATGTTCTGTAAGCGTGGACCAAGCTCACTAT 541  
QY 459 GCGCAAGAACCAATCTTTGTTTCTCCCTCCGAGTCTCTCTGATTAAAGA 509  
Db 542 GCGCAAGAACCAATCTTTGTTTCTCCCTCCGAGTCTCTGATTAAAGA 592

QY 399 AATTGCTTTGCTGCTCAGAGAGTGGAGCTGCAAAAGCGGTCTTAAACTCACTAT 458  
Db 482 AACTGCTTTGAGGCTTTAAAAAAATGTTCTGTAAGCGTGGACCAAGCTCACTAT 541  
QY 459 GCGCAAGAACCAATCTTTGTTTCTCCCTCCGAGTCTCTCTGATTAAAGA 509  
Db 542 GCGCAAGAACCAATCTTTGTTTCTCCCTCCGAGTCTCTGATTAAAGA 592

RESULT 11

US-10-280-864-1  
; Sequence 1, Application US/10280864  
; Publication No. US20030054492A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svetlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozlanov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/10/280,864  
; PRIOR FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: US/09/929,945  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized sequence for human acidic  
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
; NAME/KEY: CDS  
; LOCATION: (122)...(590)  
US-10-280-864-1

Query Match 49.2%; Score 314.2; DB 15; Length 630;  
Best Local Similarity 79.2%; Pred. No. 2.9e-95;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
QY 39 ATGCTGAAGGGGAAATACCACTTTCAGAGCTGACGAGAGTGTAACTTCCCTCCA 98  
Db 122 ATGCTGAAGGGGAAATACCACTTTCAGAGCTGACGAGAGTGTAACTTCCCTCCA 181  
QY 99 GCGAATTACAAAGAGCCCAAACTCTTCTAGTACGAGAGTGTAACTTCCCTCCA 158  
Db 182 GCGAATTACAAAGAGCCCAAACTCTTCTAGTACGAGAGTGTAACTTCCCTCCA 241  
QY 159 CTTCGGATGGCAGTGGATGGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
Db 242 CTGCGAGTGGCAGTGGATGGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 301  
QY 219 CTCAGTGGCGAAAGCGTGGGGAGGTGTATAAAGATGACGAGACTGGCCAGTACTTG 278  
Db 302 CTCTCGCGCGAAAGCGTGGAGAGGTCTATATCAAGTGCAGCGAGACTGGCCAGTACTT 361  
QY 279 GCGATGACACCGGCGGTCTTTACGGCTTCACAGACACCAAAATGAGAAATGTTGTTTC 338  
Db 362 GCGATGACACCGGCGGTCTTTATGATGGCTTCACAGAGCGCTTACGAGAAATGCTGTTT 421  
QY 339 CTGAAAGGCTGGAGGAGAACCTTACAAACCTTATATCCAGAGCATGACAGAGAG 398  
Db 422 CTGAAAGGCTAGAGAAACCTTACAAACCTTATATCCAGAGCATGACAGAGAG 481  
QY 399 AATTGCTTTGCTGCTCAGAGAGTGGAGCTGCAAAAGCGGTCTTAAACTCACTAT 458  
Db 482 AACTGCTTTGAGGCTTTAAAAAAATGTTCTGTAAGCGTGGACCAAGCTCACTAT 541  
QY 459 GCGCAAGAACCAATCTTTGTTTCTCCCTCCGAGTCTCTCTGATTAAAGA 509  
Db 542 GCGCAAGAACCAATCTTTGTTTCTCCCTCCGAGTCTCTGATTAAAGA 592

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/ TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
/
/ FILE REFERENCE, PHAGE.006A
/
/ CURRENT APPLICATION NUMBER: US/09/929,918
/
/ CURRENT FILING DATE: 2001-08-15
/
/ PRIOR APPLICATION NUMBER: 09/318,288
/
/ PRIOR FILING DATE: 1999-05-25
/
/ NUMBER OF SEQ ID NOS: 11
/
/ SOFTWARE: FastSeq for Windows Version 4.0
/
/ SEQ ID NO 10
/
/ LENGTH: 990
/
/ TYPE: DNA
/
/ ORGANISM: Artificial Sequence
/
/ FEATURE:
/
/ OTHER INFORMATION: Chemically synthesized sequence for human
/
/ OTHER INFORMATION: interferon alpha- 2b
/
/ NAME/KEY: promoter
/
/ LOCATION: (231)...(249)
/
/ NAME/KEY: CDS
/
/ LOCATION: (320)...(784)
/
/ US-09-929-918-10

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Query Match	49.2%	DB 9;	Length 990;
Best Local Similarity	79.2%	Prod. No. 3.6e-95;	
Matches 373;	Conservative	0; Mismatches 98;	Indels 0; Gaps 0;
QY	39	ATGCGCTGAAGGGGAAATACACACCTTCACAGCCCTCAGCGAGAGTTTAACTGCCTCCA	98
Db	320	ATGCGCTGAAGGGGAAATACACCTTTACCGCTTACGGAGAAATTTAACTTCGCGCC	379
QY	99	GGGAATTACAAAGAGCCCAACTCTCTACTGTGTAGCAACGGGGGCCACTTCTCTGAGATC	158
Db	380	GGGAATTACAAAAGAACCAACGCTCTTTACTGCAAGTAAAGGAGACACCTTCTGCGAAT	439
QY	159	CTTCGGGATGCGACAGTGTGGAGCGACAGGACAGGACGACAGCAATTCAGCTCGAG	218
Db	440	CTGCGAGATGCCACAGTAGATGGAGTCGGCTGCTCGACACAGCAATTCAGCTGCA	499
QY	219	CTCAGTGCGBAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTG	278
Db	500	CTTCGGCGCGAAGACCGTTGGAGAGGCTATATCAAGTCGACGGAGACTGGCCAGTACCT	559
QY	279	GCCATGGACCGAGCGGCTTTTATAGGCTCTCAGACACCAATCGAGATGTTGTC	338
Db	560	GCCATGGACCGAGTGGGCTCTGTATGGCTCTCAGAGCGCTTAAGCAAGATGCTGT	619
QY	339	CTGGAAGGCTGGAGAGACCAATTACAAACCTATATATCAAGACATGACAGAGAG	398
Db	620	CTAGAAGACTAGAGAGAAACCAATTACAAACCTATATCGAAAAACATGACAGAGAG	679
QY	399	AATTGCTTTGTGGCTCCAGAGATCGGAGCTGCAAAAGCGGCTCTTAAATCTACTAT	458
Db	680	AATCGTTGTAGGCTTTAAAAAATGGTTCTCTGTAGGTGGACACGGAATCACTAT	739
QY	459	GGCCAGAGAGCAATCTTTTCTCCCGCTGCCAGTCTCTCTGATTAAAGA	509
Db	740	GGCCAAAGAGCTATCTTTCTTGGCACTACCAAGTGAAGCTTCGACTGAGAG	90

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US 09-968-007A-133
; Sequence 133, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; TITLE OF INVENTION: Cancer Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02

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```

US-10-649-480-1
; Sequence 1, Application US/10649480
; Publication No. US20040115769A1
; GENERAL INFORMATION:
; APPLICANT: Stegmann, Thomas
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
; FILE REFERENCE: CVGENG.008A
; CURRENT APPLICATION NUMBER: US/10/649,480
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/649,480
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized sequence for human acidic
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using
; OTHER INFORMATION: preferred codons for E. coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (122)...(590)
US-10-649-480-1

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Query Match	49.2%	Score 314.2	DB 17	Length 630
Best Local Similarity	79.2%	Pred. No. 2.9e-95		
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QY	39	ATGCGCTGAAGGGGAAATACCAACCTTCACAGCGCTCAGCGAGAGTTTAAATCTCCCTCCA	98	
Db	122	ATGCGCTGAAGGGGAAATACCAACCTTCACAGCTTACGGAGAAATTTAACTTCGCGCC	181	
QY	99	GGGAATTCAGAGAGCCGAAATCTCTTACTGTGTAGACAGGGGGCCACTTCTTGAGGATC	158	
Db	182	GGGAATTTACAAAAACCCAGACTCTTCTTACTGCAAGTAAACGGAGGACACTTCTCGCAAT	241	
QY	159	CTTCGGGATGCGCACTGTGATGGGACAGGAGGACGAGCAGCACCAATTCAGCTGCGAG	218	
Db	242	CTCCAGATGCGCACTGTAGATGGGACTCGCATCGCTCGACACGCAATTTCACTGCGAA	301	
QY	219	CTCAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGGCCACTCTTG	278	
Db	302	CTCTCGGGCGGAAAGCGTTGGAGAGGCTTATATACGTGCGAGGAGCTGGCGAGTACCT	361	
QY	279	GCCATGAGACCGACGGGCTTTTATACGGCTTCACAGACACCAATGCGAGATGTTGTTC	338	
Db	362	GCCATGAGACCGATGGGCTTCTGTATGGCTCAGAGCGCTTACGAGAGATCGTTGTT	421	
QY	339	CTGGAAAGGCTGGAGGAGACCAATTAACAACCTTATATATCAAGAGCATGCGAGAAG	398	
Db	422	CTGAAGAAGCTAGAGAAGAAACCAATTACAACGTCATATCGAAAAAACAATGCGAGAAG	481	
QY	399	AATTGGTTTGTGGGCTTCAAGAAGAAATGGGAGCTGCAAAAGCGGCTCTAAACACTCACTAT	458	
Db	482	AATCGTTTGTAGGCTTTAAAAAATAATGGTTCTGTAAAGGTGGACACCGGACTCACTAT	541	
QY	459	GGCCAGAAAGCAATCTGTGTTTCTCCCGCTGCGAGTCTCTTCTGATTAAAGA	509	
Db	542	GGCCAAAGGCTATCTGTGTTCTGCGCACTACAGGTGAGCTCGGACTGAAGA	592	

US-09-929-918-10  
Sequence 10, Application US/09929918  
Patent No. US20020090678A1  
GENERAL INFORMATION:  
APPLICANT: Kordyum, Vitaliy A.  
APPLICANT: Chernykh, Svitlana I.  
APPLICANT: Slavchenko, Iryna Yu.  
APPLICANT: Vozianov, Oleksandr  
TITLE OF INVENTION: PHASE-DEPENDENT SUPER PRODUCTION OF

; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 133
; LENGTH: 3658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-133

Query Match 47.5%; Score 302.8; DB 12; Length 3658;
Best Local Similarity 96.0%; Pred. No. 4.8e-91;
Matches 332; Conservative 0; Mismatches 12; Indels 2; Gaps 2;
QY 294 GGCCTTTTATACGGCTCACAGACACCAATGAGGATGTTGTTCTGGAAGGCTGGAG 353
DB 286 GTGGTTTATCTTTTACGACACCAATGAGGATGTTGTTCTGGAAGGCTGGAG 345
QY 354 GAGACCAATTACCAACCTATATATCAAGAGCATGCAAGAGAAATGTTGTTGTCG 413
DB 346 GAGACCAATTACCAACCTATATATCAAGAGCATGCAAGAGAAATGTTGTTGTCG 405
QY 414 CTCAGAGAAATGGAGCTGCAAAACGGCTCTTAAACTCACTATGCGCAGAAAGCAATC 473
DB 406 CTCAGAGAAATGGAGCTGCAAAACGGCTCTTAAACTCACTATGCGCAGAAAGCAATC 465
QY 474 TTGTTTCTCCCTCCAGTCTCTTCTGATTAAGAGATCTGTTCT-GGTGTTGACCACT 532
DB 466 TTGTTTCTCCCTCCAGTCTCTTCTGATTAAGAGATCTGTTCTGCGGTGTTGACCACT 525
QY 533 CCAGAGAGTTTCGAGGGTCTCTCACTGTTGACCCCAAAATGTTCCCTTGACCACT 592
DB 526 CCAGAGAGTTTCGAGGGTCTCTCACTGTTGACCCCAAAATGTTCCCTTGACCACT 584
QY 593 GTCGCGCTAACCCCGAGCGCCACAGAGCTGCAATTTGTAAGCAACTT 638
DB 585 GTCGCGCTAACCCCGAGCGCCACAGAGCTGCAATTTGTAAGCAACTT 630

RESULT 15

US-09-968-007A-440
; Sequence 440, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 440
; LENGTH: 3658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-440

Query Match 47.5%; Score 302.8; DB 12; Length 3658;
Best Local Similarity 96.0%; Pred. No. 4.8e-91;
Matches 332; Conservative 0; Mismatches 12; Indels 2; Gaps 2;
QY 294 GGCCTTTTATACGGCTCACAGACACCAATGAGGATGTTGTTCTGGAAGGCTGGAG 353
DB 286 GTGGTTTATCTTTTACGACACCAATGAGGATGTTGTTCTGGAAGGCTGGAG 345
QY 354 GAGACCAATTACCAACCTATATATCAAGAGCATGCAAGAGAAATGTTGTTGTCG 413

DB 346 GAGACCAATTACCAACCTATATATCAAGAGCATGCAAGAGAAATGTTGTTGTCG 405
QY 414 CTCAGAGAAATGGAGCTGCAAAACGGCTCTTAAACTCACTATGCGCAGAAAGCAATC 473
DB 406 CTCAGAGAAATGGAGCTGCAAAACGGCTCTTAAACTCACTATGCGCAGAAAGCAATC 465
QY 474 TTGTTTCTCCCTCCAGTCTCTTCTGATTAAGAGATCTGTTCT-GGTGTTGACCACT 532
DB 466 TTGTTTCTCCCTCCAGTCTCTTCTGATTAAGAGATCTGTTCTGCGGTGTTGACCACT 525
QY 533 CCAGAGAGTTTCGAGGGTCTCTCACTGTTGACCCCAAAATGTTCCCTTGACCACT 592
DB 526 CCAGAGAGTTTCGAGGGTCTCTCACTGTTGACCCCAAAATGTTCCCTTGACCACT 584
QY 593 GTCGCGCTAACCCCGAGCGCCACAGAGCTGCAATTTGTAAGCAACTT 638
DB 585 GTCGCGCTAACCCCGAGCGCCACAGAGCTGCAATTTGTAAGCAACTT 630

Search completed: August 24, 2004, 21:00:18
Job time : 484 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 18:35:10 ; Search time 2845 Seconds
(without alignments)
6696.686 Million cell updates/sec

Title: US-10-022-554A-3
Perfect score: 638
Sequence: 1 gaattcggaacgcgcaca.....cctgaattgtaagcaactt 638

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estma:\*
- 5: em\_estov:\*
- 6: em\_estro:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pin:\*
- 20: em\_gss\_vit:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_pig:\*
- 27: em\_gss\_vit:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	601.8	94.3	1173	13	BX444567	BX444567 BX444567	
2	576.8	90.4	832	12	B1869731	B1869731 603339366	
3	569.4	89.2	1057	13	BQ067949	BQ067949 AGENCOUR	
4	567	88.9	1014	12	BM809005	BM809005 AGENCOUR	
5	560.8	87.9	878	12	B1753845	B1753845 60302755	
6	559.8	87.7	821	12	B1598390	B1598390 603250005	
c	511.4	80.2	534	9	AI590078	AI590078 tms8c01.x	
8	501.6	78.6	714	12	BG706412	BG706412 60266974	
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11	425.4	66.7	843	12	B1692283	B1692283 603342755	
12	424.2	66.5	461	10	BF956865	BF956865 RC1-NN020	
13	420.6	65.9	2706	11	B027001	B027001 Mus musc	
14	408.2	64.0	663	9	AI119291	AI119291 ue95c07.y	
15	404	63.3	855	12	B1331990	B1331990 602984395	
c	402.2	63.0	750	13	B0627243	B0627243 UI-H-FGC	
17	401.2	62.9	508	29	C9633840	C9633840 OST35398	
18	385.4	60.4	526	29	C0565930	C0565930 OST19113	
19	385.2	60.4	631	10	B8677624	B8677624 CGS65330	
20	385.2	60.4	689	9	AI663400	B8677624	
21	356	55.8	813	10	BF532970	BF532970 uk32d07.y	
22	354.6	55.6	611	13	BH840197	BF532970 60207349	
c	328.6	51.5	386	10	BF956862	BH840197 AGENCOUR	
24	327.4	51.3	485	10	BF442355	BF956862 CM3-NN02	
25	323.6	50.7	485	29	C0554707	BF442355 259038 M	
26	320.6	50.3	522	14	CD701495	C0554707 OST176859	
27	316.8	49.7	529	29	C0629018	CD701495 EST18019	
28	316.6	49.6	543	9	AA261582	C0629018 OST340659	
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c	302	47.3	701	12	BM959210	CB773841 MGNNUC1	
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33	291.4	45.7	570	12	B1598882	BM364489 BS3000090	
c	281	44.0	458	9	AA594274	B1598882 60324798	
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c	279	43.7	415	9	AI083919	BA488304 DKP26866	
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44	247	38.7	436	10	BB850804	CG613113 OST279910	
45	246	38.6	329	29	CG496943	BB850804 BB850804	
						CG496943 OST37278	

## ALIGNMENTS

RESULT 1	
BX444567	
LOCUS	1173 bp mRNA linear EST 15-MAY-2003
DEFINITION	BX444567 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
	CSODN003VP16 5'-PRIME, mRNA sequence.
ACCESSION	BX444567
VERSION	BX444567.1 GI:30780253
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1173)
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope

Genoscope - Centre National de Sequençage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 3201.r For  
more information about this cluster, see  
[http://www.genoscope.cns.fr/  
csi-biag/cluster.cgi?seq=CSODN003DH080Fl&cluster=3201.r](http://www.genoscope.cns.fr/csi-biag/cluster.cgi?seq=CSODN003DH080Fl&cluster=3201.r). Contact :  
Peng Liang Email : [liang@life.technologies.com](mailto:liang@life.technologies.com) URL :  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSODN003DH080Fl.

## FEATURES

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1. 1173
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDN003XP16"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone.lib="Homo sapiens ADULT BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. library was not normalized."

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## ORIGIN

Query Match 94.3%; Score 601.8; DB 13; Length 1173;  
Best Local Similarity 98.6%; Pred. No. 6.9e-166;  
Matches 628; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY	3	ATTCGGGAACGGCCCAAGACAGCAGCTCTGAGCCATCGCTGAAAGGGAATCACCACC	62
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QY	123	CTCTACTGTAGCAACGGGGGCCATTTCTGAGGATCTTCCGATGGCACAGTGGATGG	182
Db	252	CTCTACTGTAGCAACGGGGGCCATTTCTGAGGATCTTCCGATGGCACAGTGGATGG	311
QY	183	ACAAGGACAGAGCGACACACATTTACAGCTGCAGCTCAGTGCGAAGCGTGGGGAG	242
Db	312	ACAAGGACAGAGCGACACACATTTACAGCTGCAGCTCAGTGCGAAGCGTGGGGAG	371
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QY	303	TAGGCTCACAGACACAAATGAGAAATGTTTGTCTGGAAGGCTGGAGAGAACCAT	362
Db	432	TAGGCTCACAGACACAAATGAGAAATGTTTGTCTGGAAGGCTGGAGAGAACCAT	491
QY	363	TACAACACTATATATCCAGAAGACATCGACAGAAATGTTTGTGGCCTCAGAG	422
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QY	423	AATGGGAGCTGMAAGGGTCTTAAACTCATTATGSCCAGAAAGCAATCTGTGTTCTC	482
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QY	483	CCCTGCGCACTCTCTCTGATATAAGAGATCTGTTCT-GGTGTGACCACCTCCACAGAG	541
Db	612	CCCTGCGCACTCTCTCTGATATAAGAGATCTGTTCTGCGGTGTGACCACCTCCACAGAG	671
QY	542	TTTCGAGGGTCTCAGCTGGTTGACCCCAAAATGTTCCTTGACATTTGGCTCGGCTA	601
Db	672	TTTCGAGGGTCTCAGCTGGTTGA-CCAAAATGTTCCTTGACCAATTTGGCTCGGCTA	730
QY	602	ACCCCGAGCCACAGAGCTGAAATTTGAGCAACTT	638
Db	731	ACCCCGAGCCACAGAGCTGAAATTTGAGCAACTT	767

## RESULT 2

BI869731

**LOCUS**

BI869731 832 bp mRNA linear EST 11-OCT-2001

DEFINITION 603393620F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:5403677 5', mRNA sequence.

ACCESSION B1869731

VERSION B1869731.1 GI:16043404

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 832)

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgsbbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM12029 row: 9 column: 06  
High quality sequence stop: 829.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5403677"  
/tissue\_type="adenocarcinoma, cell line"  
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/clone\_lib="NIH\_MGC\_90"  
/note="Organ: liver; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

FEATURES  
source  
Query Match 90.4%; Score 576.8; DB 12; Length 832;  
Best Local Similarity 98.3%; Pred. No. 1.4e-158;  
Matches 625; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

QY 5 TCGGACGCGCCACAGCAGCAGCTCTGAGCCATGGCTGAAAGGGGAAATCACCACCTT 64

Db TCTTGAAGCGCCACAGCAGCAGCTCTGAGCCATGGCTGAAAGGGGAAATCACCACCTT 105

QY 65 CACAGCCCTGACGAGAGTTTAACTGCTCCAGGGAATTACAGAGCCCAACTCTCT 124

Db CACAGCCCTGACGAGAGTTTAACTGCTCCAGGGAATTACAGAGCCCAACTCTCT 165

QY 125 CTACTGTAGCAACCGGGGCCACTCTCTGAGGATCTTCGAGATGGCAGCATGTGGGAC 184

Db CTACTGTAGCAACCGGGGCCACTCTCTGAGGATCTTCGAGATGGCAGCATGTGGGAC 225

QY 185 AAGGACAGGAGCAGCAGCAGCTTCACTGCTGAGCTCAGTGCAGGAGCGTGGGAGGT 244

Db AAGGACAGGAGCAGCAGCAGCTTCACTGCTGAGCTCAGTGCAGGAGCGTGGGAGGT 285

QY 245 GTATATAAGAGTACCGAGACTGCGCATGTTGCGCATGAGCAGCAGCGGCTTTTATA 304

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QY 305 CGGCTCAGACACCAATAGGAATGTTTCTCTGGAAGGCTGGAGGAGACCATTA 364

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QY 365 CACACCTTATATTCAGAGAGCATGACAGAGAAATGTTTGTGGCTCTCAAGAGAA 424

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QY 425 TGGAGCTGCAAA - CGCGGTCTTAAACTCACTATGCGCGAAGCAATCTGTTTCTCC 483

Db TGGAGCTGCAAA - CGCGGTCTTAAACTCACTATGCGCGAAGCAATCTGTTTCTCC 524

QY 484 CCTGCCAGTCTCTCTGATTTAAAGAGATCTGTTCT - GGTGTTGACCACTCCAGAGAA 542

Db CCTGCCAGTCTCTCTGATTTAAAGAGATCTGTTCTGTTGTTGATGACCACTCCAGAGAA 584

QY 543 TTCAGGGGTCTCCTCCTGTTGACCCCAAAATGTTCCCTTGACCAATGCTGCGCTAA 602

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QY 603 CCCACAGCCACACAGCAGCTGAAATTTGTAAGCACTT 638

Db CCCACAGCCACACAGCAGCTGAAATTTGTAAGCACTT 679

RESULT 3

LOCUS BQ067949

DEFINITION AGENCOURT\_6792377 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5768943

5', mRNA sequence.

ACCESSION BQ067949

VERSION BQ067949.1 GI:19896995

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 1057)

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgsbbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM12829 row: j column: 16  
High quality sequence stop: 470.  
Location/Qualifiers  
1. .1057  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:5768943"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_121"  
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned. EcoRV site is destroyed upon cloning. Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH\_MGC Library."

FEATURES  
source  
Query Match 89.2%; Score 569.4; DB 13; Length 1057;  
Best Local Similarity 96.2%; Pred. No. 2.4e-156;  
Matches 615; Conservative 0; Mismatches 21; Indels 3; Gaps 3;

QY 3 ATTCGGGACCGCCACAGCAGCAGCTCTGAGCCATGGCTGAAAGGGGAAATCACCACC 62

Db AGTCTTGAAGCGCCACAGCAGCAGCTCTGAGCCATGGCTGAAAGGGGAAATCACCACC 164

QY 63 TTCACAGCCCTGACCGAGAGTTTAACTGCTCCAGGGAATTACAGAGCCCAACTC 122

Db TTCACAGCCCTGACCGAGAGTTTAACTGCTCCAGGGAATTACAGAGCCCAACTC 224

QY 123 CTCTACTGTAGCAACCGGGGCCACTTTCTCTGAGGATCTTTCGCGATGGCAGATGGATGG 182

Db CTCTACTGTAGCAACCGGGGCCACTTTCTCTGAGGATCTTTCGCGATGGCAGATGGATGG 284

QY 183 ACAAGGACAGCAGCAGCAGCATTCAGCTCAGCTCAGTTCGCGAAAGCGTGGGGAG 242

Db ACAAGGACAGCAGCAGCAGCATTCAGCTCAGCTCAGTTCGCGAAAGCGTGGGGAG 344

QY 243 GTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGACACCGCGGCTTTTA 302

ORIGIN

Query Match 89.2%; Score 569.4; DB 13; Length 1057;  
Best Local Similarity 96.2%; Pred. No. 2.4e-156;  
Matches 615; Conservative 0; Mismatches 21; Indels 3; Gaps 3;

QY 3 ATTCGGGACCGCCACAGCAGCAGCTCTGAGCCATGGCTGAAAGGGGAAATCACCACC 62

Db AGTCTTGAAGCGCCACAGCAGCAGCTCTGAGCCATGGCTGAAAGGGGAAATCACCACC 164

QY 63 TTCACAGCCCTGACCGAGAGTTTAACTGCTCCAGGGAATTACAGAGCCCAACTC 122

Db TTCACAGCCCTGACCGAGAGTTTAACTGCTCCAGGGAATTACAGAGCCCAACTC 224

QY 123 CTCTACTGTAGCAACCGGGGCCACTTTCTCTGAGGATCTTTCGCGATGGCAGATGGATGG 182

Db CTCTACTGTAGCAACCGGGGCCACTTTCTCTGAGGATCTTTCGCGATGGCAGATGGATGG 284

QY 183 ACAAGGACAGCAGCAGCAGCATTCAGCTCAGCTCAGTTCGCGAAAGCGTGGGGAG 242

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Db 585 CCCCTGCGAGTCTCTCTGATTAAGAGATCTGTCTGAGGTGTGACCACTCCAGAA 644  
QY 541 GTTTCAGGGGCTCTCACTGCTGACCCCAAAATGTTCCTTGACCACTGCGGCT 600  
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Db 705 AACCCCGCCAGAGAGCGCTGAAATTTGTAAGCAACTT 743

RESULT 4  
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LOCUS  
DEFINITION  
AGENCOURT\_6617747 NIH\_MGC\_124 Homo sapiens cDNA clone IMAGE:573445  
5', mRNA sequence.  
ACCESSION  
BM809005  
VERSION  
BM809005.1 GI:19125828  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1014)  
TITLE  
NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL  
National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Invitrogen  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Cloned Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL2739 row: m column: 06  
High quality sequence stop: 637.

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Location/Qualifiers  
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/clone\_lib="NIH\_MGC\_124"  
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(destroyed); Site 2: NotI; RNA source male hippocampus,  
age 27. Library is oligo-dT primed and directionally  
cloned (EcoRV site is destroyed upon cloning). Average  
insert size 1.4 kb. Insert size range 0.9-4 kb. Library is  
normalized and enriched for full-length clones and was  
constructed by C. Gruber (Invitrogen). Research Genetics  
tracking code 012."

ORIGIN  
Query Match 88.9%; Score 567; DB 12; Length 1014;  
Best Local Similarity 97.0%; Pred. No. 1.2e-155;  
Matches 610; Conservative 0; Mismatches 15; Indels 4; Gaps 3;  
QY 3 ATTGGGACCGCCCAAGCAGCAGCTGTGTGAGCCATGCTGAAGGGGAAATCACCACC 62

Db 147 AGTCTTGAAGCGCCACAGCAGCAGCTGTGAGCCATGAGGGAATCACCACC 206  
QY 63 TTACAGAGCCCTACCCAGAGAGTTTAACTCTGCTCCAGGGAATACAGAGGCCCAACTC 122  
Db 207 TTACAGAGCCCTACCCAGAGAGTTTAACTCTGCTCCAGGGAATACAGAGGCCCAACTC 266  
QY 123 CTCTACTGTAGCAACCGGCGGCACTTCTCTGAGGATCTTCCGGATGGCACAGTGGATGG 182  
Db 267 CTCTACTGTAGCAACCGGCGGCACTTCTCTGAGGATCTTCCGGATGGCACAGTGGATGG 326  
QY 183 ACAAGGACAGAGCGGACCCAGCAGCATTTGAGCTGCTGAGTGGAGAGGCTGGAGAGGAG 242  
Db 327 ACAAGGACAGAGCGGACCCAGCAGCATTTGAGCTGCTGAGTGGAGAGGCTGGAGAGGAG 386  
QY 243 GTGTATTAAGAGATACGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGGCTTTTA 302  
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QY 303 TAGCGCTCAGACAGACCAAAATAGGAATTTTGTCTGAGGATCTTCCGGATGGCACAGTGGATGG 362  
Db 447 TAGCGCTCAGACAGACCAAAATAGGAATTTTGTCTGAGGATCTTCCGGATGGCACAGTGGATGG 506  
QY 363 TACACACCTATATATCAAGAGCATSCAGAGAGAAATGGTTTGGCTCAAGAAG 422  
Db 507 TACACACCTATATATCAAGAGCATSCAGAGAGAAATGGTTTGGCTCAAGAAG 566  
QY 423 AATGGAGCTGCAAAAGCGGCTTAAACTCACTATGGCCAGAAAGCAATCTTTTCTC 482  
Db 567 AATGGAGCTGCAAAAGCGGCTTGGACTCTGAGTCTGAGTGGCCAGAAAGCAATCTTTTCTC 626  
QY 483 CCCCTGCGAGTCTCTCTGATTAAGAGATCTGTCT- GGTGTGACCACTCCAGAGAA 541  
Db 627 CCCCTGCGAGTCTCTCTGATTAAGAGATCTGTCTGGGTGTGACCACTCCAGAGAA 686  
QY 542 TTTCGA- GCGGTCTCACTGCTGACCCCAAAATGGTTTGGCTTGGCAATGGCTGGC 599  
Db 687 GTTCGAGGGGGGTCTCACTGCGTGGCCCAAAATGGTTTGGCAATGGCTGGC 746  
QY 600 TAAACCCCGCCAGAG- CACAGAGCGCTGAATTT 627  
Db 747 TAAACCCCGCCAGAGCGGCTGAAATTT 775

RESULT 5  
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LOCUS  
DEFINITION  
60302526F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5197783 5',  
mRNA sequence.  
ACCESSION  
BM809005  
VERSION  
BM809005.1 GI:15745423  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 878)  
TITLE  
NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL  
National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Cloned Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL1495 row: d column: 08  
High quality sequence stop: 703.

FEATURES  
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/clone\_lib="NIH\_MGC\_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 87.9%; Score 560.8; DB 12; Length 878;  
Best Local Similarity 96.6%; Pred. No. 7.3e-154;  
Matches 604; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

QY 3 ATTGGGAGCGCCCAACAGCAGCTGCTGAGCCATGCTGAAGGGGAAATCACACC 62  
DB 81 ANTCCTGAAAGCGCCCAACAGCAGCTGCTGAGCCATGCTGAAGGGGAAATCACACC 140  
QY 63 TTCACAGCCCTGACGAGAGTTAATCCCTCCAGGGAATTTACAGAGCCCAAA-CT 121  
DB 141 TTCACAGCCCTGACGAGAGTTAATCCCTCCAGGGAATTTACAGAGCCCAAAAGCT 200  
QY 122 CTTCTACTGTAGCAACGGGGGCACTTCTGAGGATCTTCCGAGTGCACAGTGGATGG 181  
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QY 182 GACAGAGGACAGAGCGGACGACATTCAGCTGCGAGTCCAGTCCGAGAGGTGGGGGA 241  
DB 261 GACAGAGGACAGAGCGGACGACATTCAGCTGCGAGTCCAGTCCGAGAGGTGGGGGA 320  
QY 242 GGTGTATATAAGAGTACGAGAGCTGCGAGTCTTGGCCATGACACGAGCGGCTTTT 301  
DB 321 GGTGTATATAAGAGTACGAGAGCTGCGAGTCTTGGCCATGACACGAGCGGCTTTT 380  
QY 302 ATACGGCTCAGACACCAATAGAGTGTGTTCTTGGAGGATGCTGAGAGGCTGGAGAGCA 361  
DB 381 ATACGGCTCAGACACCAATAGAGTGTGTTCTTGGAGGATGCTGAGAGGCTGGAGAGCA 440  
QY 362 TTACACACCTATATATACAGAGGATGCGAGAGATTTGGTTGGCTTCAAGAA 421  
DB 441 TTACACACCTATATATACAGAGGATGCGAGAGATTTGGTTGGCTTCAAGAA 500  
QY 422 GAATGGAGCTGCAACCGGGTCTTAAATCTACTATGCGAGAGGCAATCTGTTTCT 481  
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DB 561 CCCCCTGCCAGTCTTCTGATTAAGAGATCTTCTGTTGTTGACCACTCCAGAGAG 620  
QY 542 TTTCAGGGGCTCTCACTGCTGACCCCAAAATGTTCCCTGAGCAATCTGCTGCGCTA 601  
DB 621 TTTCAGGGGCTCTCACTGCTGACCCCAAAATGTTCCCTGAGCAATCTGCTGCGCTA 679  
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DB 680 ACCCCAG-CCACAGAGCTGAAAT 703

RESULT 6  
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LOCUS  
DEFINITION B1598390 821 bp mRNA linear EST 07-SEP-2001  
mRNA sequence.  
ACCESSION B1598390  
VERSION B1598390.1 GI:15491329  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 821)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgsaps-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUMI)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLUMI at: <http://image.llnl.gov>  
Plate: LLAM11764 Row: k Column: 23  
High quality sequence stop: 777.  
Location/Qualifiers

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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (Gcgag); Oligo-dT primed using primer 5'-TTTCTTTTCTTTT-3', size-selected for average insert size 2.3 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 87.7%; Score 559.8; DB 12; Length 821;  
Best Local Similarity 95.3%; Pred. No. 1.4e-153;  
Matches 609; Conservative 0; Mismatches 27; Indels 3; Gaps 3;

QY 3 ATTGGGAGCGCCCAACAGCAGCTGCTGAGCCATGCTGAAGGGGAAATCACACC 62  
DB 114 AGTCTTGAAGCGCCCAACAGCAGCTGCTGAGCCATGCTGAAGGGGAAATCACACC 173  
QY 63 TTCACAGCCCTGACGAGAGTTAATCCCTCCAGGGAATTTACAGAGCCCAAACTC 122  
DB 174 TTCACAGCCCTGACGAGAGTTAATCCCTCCAGGGAATTTACAGAGCCCAAACTC 233  
QY 123 CTTCTACTGTAGCAACGGGGGCACTTCTGAGGATCTTCCGAGTGCACAGTGGATGG 182  
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QY 183 ACAGAGGACAGAGGAGCAGACATTCAGCTGAGTCCAGTCCAGAGGCTGGGGGAG 242  
DB 294 ACAGAGGACAGAGGAGCAGACATTCAGCTGAGTCCAGTCCAGAGGCTGGGGGAG 353  
QY 243 GTGTATATAAGAGTACCGAGCTGCGAGTACTTGGCCATGCGACCGCGGCTTTTA 302  
DB 354 GTGTATATAAGAGTACCGAGCTGCGAGTACTTGGCCATGCGACCGCGGCTTTTA 413  
QY 303 TACGGCTCAGACAGACCAATGAGGAATTTGTTCTGGAAGGCTGGAGAGAACAT 362  
DB 414 TACGGCTCAGACAGACCAATGAGGAATTTGTTCTGGAAGGCTGGAGAGAACAT 473  
QY 363 TACACACCTATATATCCAGAGCATGCGAGAGAAATTTGTTGCTGCTCAGAGAG 422  
DB 474 TACACACCTATATATCCAGAGCATGCGAGAGAAATTTGTTGCTGCTCAGAGAG 533  
QY 423 AATGGAGCTGCAACCGGGTCTTAAACTCACTATGCGCAAGAGCAATCTGTTTCTC 482  
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DB 594 CCCCCTGCCAGTCTTCTGATTAAGAGATCTGTTCTGTTGTTGACCACTCCAGAGAG 653  
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DB 714 ATCCCCAGCCCAACAGAGGCTGCAATTTGTGAAGCACTT 752

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 (HUMAN); mRNA sequence.

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 Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

mammalia; Euterria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 534)  
NCBI/NIHDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BrGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strawn, PhD

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
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High quality sequence stop: 455.

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strand cDNA was primed with a Not I - oligo(dT) primer [5], TGTACCAATCTTAAGTGGCGGCGGCGATAGTCTTTTCTTTTCTTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV73 vector. Library is normalized, and was constructed by Bento Soares and M.Fátima Bonaldo."

h 80.2% Score 511.4; DB 9; Length 534;  
Similarity 98.7%; Pred. No. 2.le-139;  
28; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

[illegible]

GCCTCACCAGAAATTAAATCTGCTTCCAGGGAATTACAAGGCCCAACTCTCTAC 415  
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9 GACGACGAGCACCAGCACATTCACGCTGCACGCTCAGTTCGGGAAGCGTGCGGGAGAGTGTAT 248  
 1 GACGACGAGCAGCACGACGACATTCACGCTGCACGCTCAGTTCGGGAAGCGTGCGGGAGAGTGTAT 295

3 ATAAAGAGTACCGAGACTTGGCCAGTACTTGGCCATCGACACCGAGGGCTTTTATACGC 308  
 4 ATAAAGAGTACCGAGACTTGGCCAGTACTTGGCCATCGACACCGAGGGCTTTTATACGC 235  
 5 TCACAGACACCAATATGAGGAATGTTTGTCTCGAAAGCTGGAGGAGAACCAATTACAAC 368

[illegible]

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QY	369	ACCTATATATCCAGAAGCATGCGAGAGAAATGGTTTGGGCTCAAGAAGATGGG	428
Db	174	ACCTATATATCCAGAAGCATGCGAGAGAAATGGTTTGGGCTCAAGAAGATGGG	115
QY	429	AGCTGCAAAACGGGCTCTAAACTACTATGSCAGAAAGCAATCTTGTTTCTCCCCCTG	488
Db	114	AGCTGCAAAACGGGCTCTGGACTCATATGCGCAAGAGCAATCTTGTTTCTCCCCCTG	55
QY	489	CAAGTCTCTCTGATTAAGAGATCTGTCTCTGGTGGACCACTCCAGAGAA	540
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RESULT 8	714 bp	mRNA	linear	EST 07-MAY-2007
BG706412				
LOCUS	BG706412			

DEFINITION	602669744F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792378 5', mRNA sequence.
ACCESSION	BG706412
VERSION	BG706412.1 GI:13981735
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

ORGANISM Homo sapiens (human)

Euarchyot: Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 714)

NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.

REFERENCE

AUTHORS

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA library preparation: Michael J. Brownstein (MGBRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:

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http://image.llnl.gov
Plate: LLAM10670 row: h column: ll
High quality sequence stop: 710.
Location/Qualifiers
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        1. 714

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/Clone_lib="NIH_MGC_96"
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5'-TTTTTTTTTTTTTTT-3', size-selected for average

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insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NIHRI, National Institutes of Health). Note: this is a NIH/NIHRI library.

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ORIGIN
      78.6%;   Score 501.6;   DB 12;   Length 714;
Best local similarity 96.5%;   Pred. NO. 1.9e-136;
Matches 577;   Conservative 0;   Mismatches 14;   Indels 7;   Gaps 5.

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3 ATTGGGAACGCGCCACAAGCAGCAGCTGTCTAGCATGGCTGAAGGCGAAATCACACC 62  
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 114 AGTCTTAAGGCGCCACAAGCAGCAGCTGTCTAGCATGGCTGAAGGCGAAATCACACC 173

63 *ITCAGGCUCTACCGAGAGTTTAACTCTGCTTCAGGGAATTACAAGAGCCCAAACTC* 132  
174 *TTTCACGCCCTTACCGAGAGATTGTTAACTCTGCTTCCA-GGAAATTACAAGAGCCCAAACTC* 232  
123 *CTCTACTGTAGCAACGGGGGCCACTTCTCTGAGATCTCTCCGAGTGGCAGCATGGTGGTGG* 182

233 CTCTACTGTAGCAACGGGGGCCACTTCTGAGGATCCTTCGGGATGGCACA GTGGATGGG 232

Best Local Similarity	96.8%;	Pred. No. 1.1e-117;
Matches	457;	Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY	68	AGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATACAAAGCCCAACCTCTCTCTA 127
Db	472	AGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATACAAAGCCCAACCTCTCTCTA 413
QY	128	CTGTAGCAACCGGGGGCCACTCTCTGAGGACTCTTCGGATGGCAGACGTGCTGCGACAAG 187
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QY	198	GGACAGGAGCGACACGACACATTGACGTGACGCTAGTGGCGAAAGCGTGGGGGAGGTGTA 247
Db	352	GGACAGGAGCGACACGACACATTGACGTGACGCTAGTGGCGAAAGCGTGGGGGAGGTGTA 293
QY	248	TATAAAGAGTACCGAGACTGGCGACGTACTTGGCCATGACACCGACGGGCTTTTATACGG 307
Db	292	TATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGACACCGACGGGCTTTTATACGG 233
QY	308	CTCAGAGACACCAATATGAGGAATGTCTTCTCGAAGAGCGTGGAGAGAACCATTCACAA 367
Db	232	CTCAGAGACACCAATATGAGGAATTTTTTGTCTCGGAGGGGCTGGAGAGAACCATTCACAA 173
QY	368	CACCTATATATCCAAAGAGCATCGAGAGAAGATTGGTTTGTTCGCTTCAAGAAGATGG 427
Db	172	CACCTATATATCCAAAGAGCATCGAGAGAAGATGGTTTGTTCGCTTCAAGAAGATGG 113
QY	428	GAGCTGCAAAACGGGTCTTAAACTCATATGGCCAGAAAGCAATCTGTGTCTCCGCT 487
Db	112	GAGCTGCAAAACGGGTCTCGACTCATATGGCCAGAAAGCAATCTGTGTCTCCGCT 53
QY	488	CCGAGTCTCTCTGATTAAGAGATCTGTCTT-GGTGTGACCACTCCAGAG 538
Db	52	GCGAGTCTCTCTGATTAAGAGATCTGTCTGGGTGTTCAGCACTCCAGAG 1

Db 112 GAGCTGAAACGGGTCTCGAGCTACTATGCGCAAGAGCAATCTGTCTCCCOCT 53

OY 488 GCCAGTCTCTCTGATTAAGAGATGCTGTCT-GGTGTGACCACTCCAGAG 538

Db 52 GCCAGTCTCTCTGATTAAGAGATGCTGTCTGGGTGTTCACCACTCCAGAG 1

RESULT 10	
AK035330	
LOCUS	3404 bp mRNA linear HTC 18-SEP-2003
DEFINITION	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530018E22 product:fibroblast growth factor 1, full insert sequence.
ACCESSION	AK035330
VERSION	AK035330.1 GI:26330609
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)

REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED

Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PubMed	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuurai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuki, M., Itoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuur, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	Riken integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multipicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913

REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

**FUNCTIONAL ANNOTATION OF A FULL-LENGTH MOUSE cDNA COLLECTION**  
 Nature 409, 685-690 (2001)  
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 3404)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohtsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tanaka, A., Takahashi, F., Takaku, Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/.  
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 /sex="male"  
 /tissue type="urinary bladder"  
 /clone lib="RIKEN full-length enriched mouse cDNA library"  
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 DB 178 GTGCGGAGCCATGCTGAGAGGAGGAGATCCACCTTACAGCCCTGACCGAGAGTTTA 237  
 QY 88 ATCTGCTTCCAGGGAATACAGAGCCCAACCTCTCTTCTAGTACAGCCGGGGCCACT 147  
 DB 238 ACCTGCTCTAGGAATACAGAGCCCAACCTCTCTTCTAGTACAGCCGGGGCCACT 297  
 QY 148 TCTGAGATCTCTGAGTGGCAGCATGTGATGGACAGGAGGAGGAGGAGGAGGAGGAG 207  
 DB 298 TCTTGGATCTCTTCTGATGGACCGTGGATGGACAGGAGGAGGAGGAGGAGGAGGAG 357

QY 208 TTCAGTCTGACCTCACTGCGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTG 267  
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 QY 268 GCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCACAGACACCAAAATGAG 327  
 DB 418 GCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCGAGACACCAAAATGAG 477  
 QY 328 AATGTTCTGCTCGAAAGGCTTGAGGAGACACCTTACACACCTATATATCCAGAAGC 387  
 DB 478 AATGTTCTGCTCGAAAGGCTTGAGGAGACACCTTATTAACACCTTACACCTCCCAAGAGC 537  
 QY 388 ATCCAGAGAGAAATTTGGTTTGTGGCTCAAGAGAAATGGGAGCTCCAAAGCGGCTCTA 447  
 DB 538 ATCCAGAGAGAAATTTGGTTTGTGGCTCAAGAGAAATGGGAGCTTGAGCGCGGCTCTC 597  
 QY 448 AATCTCATATGCGCAGAAAGCAATCTGTTTCTCCCTGCCAGCTCTCTTCTGATTTAA 507  
 DB 598 GGACTCATATGCGCAGAAAGCAATCTGTTTCTCCCTGCCAGCTCTCTTCTGATTTAA 557  
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 QY 568 CCCAAATATGTTCTTACCATTTGGCTGGCTTAACCCCGAGCCCAAGAGCCCTGAATTT 627  
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 QY 628 GTAAGCA 634  
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 B1692283  
 LOCUS 603342751P1 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5370612 5', mRNA sequence.  
 DEFINITION  
 ACCESSION B1692283  
 VERSION B1692283.1 GI:15634912  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM11943 row: e column: 13  
 High quality sequence stop: 800.  
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 /tissue type="tumor, biopsy sample"  
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 /clone lib="NCI\_CGAP Mam2"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"  
 ORIGIN  
 Query Match 66.7%; Score 425.4; DB 12; Length 843;  
 Best Local Similarity 84.5%; Pred. No. 6.1e-114;

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Dd	178	CTGTGCCAGCCNTGGCTGAAGGGGAGATCAACCTTTCAGAGCCTGCACCGAGSGTTCA	237							
Qy	88	ATCTGTCTTCAGAGGAATTACAAGAGCCGCAACTTCCTCTTGATGTGATCAAGCCCCCATCTAAT	279							

[illegible]

Db  
416 GCCAGTACTTGGCCATGGACACCGAAGGGCTTTTATACGGCTCGCAGACACCAAATGAGG 475

**QY** 328 AATGTTGTCTCTGGAAGGCGTGGAGGACCATTAACAACCTATATTATCCAGAAGC 387  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
**Db** 476 AATGTCGTCTCTGGAAGGCGTGGAGGAAACCATTATAACACTTACACCTCCAAGAAGC 535

388 ATGCAGAGAGAAGAAITGGTTTGTGGCCCTCAAGAAGAAATGGGAGCTCGAAGACGGGTCTTA 447

[illegible][illegible][illegible]

Dbb

568 CCCAAAATGTTCCCTTGACCAATTGGCTGCGCTAACCCAGCCACAGAGCCTGAATT 627

Db  
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628 GIAAGCA 634

## CONCLUSIONS

## RESULT 12

LOCUS	BF956865	461 bp	mRNA	linear	EST 22-JAN-2001
DEFINITION	BC1-NN0222	221700	073	112	112

ACCESSION	BF956865
VERSION	BF956865.1 GI:12374140

SOURCE	Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
1 (bases 1 to 461)  
AUTHORS  
Dias Neto E  
Carcia Correa P

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Raia, G.S., Simpson, D.V.

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Jongeneel, C.V.,

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE  
20202663

FORMED  
10737800  
COMMENT  
Contact: Simpson A.J.G.

**Ludwig Institute for Cancer Research**

Brazil

**Fax: +55-11-2707001**  
**Email: [asimmons@ludwig.com.br](mailto:asimmons@ludwig.com.br)**

this sequence was derived from the FAPESP/LICR Human Cancer Genome

Db	406	GCAGTACTTGGCCATGACACCGAGGGCTTTATACGGCTCGCAGACACCAATGAGG	465
Qy	328	AAATGTTGTTCTCGAAGAAGCTCGAGAGAACCATTAACAACCTATATATCCAGAAGC	387
Db	466	AAATGTTGTTCTCGAAGAAGCTCGAGAGAACCATTAACAACCTATATCCAGAAGC	525
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Db	526	ATGCGAGAAGAACTGGTTTGTGTGGCCTCAAGAGAAGGAGAGCTGTAGCGCGTCTTC	585
Qy	448	AAATCTGACTATGCGCAGAAAGCAATCTGTTTCTTCGCCCTGCGCAGTCTCTCTGATTA	507
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Qy	568	CCCAAAATGTCTCCCTGACATTTGGCTGGCTTAACCCCCAGGCCACAGAGCTGTAATTT	627
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ACCESSION	AI119291		
VERSION	AI119291.1	GI:3519615	

SOURCE	ORGANISM
Mus musculus (house mouse),	
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
	1 (bases 1 to 663)
	Maria M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
	Colson S., Knecht M.,
	GenSeq

**TITLE**  
 The WashU-HHMI Mouse EST Project  
**JOURNAL**  
 Unpublished (1996)  
**COMMENT**  
 Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine<sup>2</sup>  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: [mousestewatson.wustl.edu](mailto:mousestewatson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:936464  
Seq primer: custom primer used  
High quality sequence spot: 537

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                sites of the pME18s-FL3 vector (5' site CACTGTTG, 3' site
                CACCATGG). XhoI should be used to isolate the cDNA
                insert since the XhoI site is present in the vector."
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<1.5kb. Library constructed by Dr. Sumio Sugano  
(University of Tokyo Institute of Medical Science).  
Custom primers for sequencing: 5' end primer  
CTTCTGCTTAAAGCTGGG and 3' end primer  
CGACTGAGCTCGAGCACA."

ORIGIN

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QY 508 GAGTCTGTTCTG 520  
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RESULT 15

BI331990  
LOCUS 602984393F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5137246 5',  
DEFINITION mRNA sequence.  
ACCESSION BI331990  
VERSION BI331990.1 GI:15016647  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1. (bases 1 to 855)  
NIH-MGC <http://mgs.cni.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL1337 row: i column: 23  
High quality sequence stop: 752.

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Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN

Query Match 63.3%; Score 404; DB 12; Length 855;  
Best Local Similarity 89.7%; Pred. No. 1.3e-107;  
Matches 434; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
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QY 208 TTCAAGCTGCAAGCTCAGTGGCGGAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTG 267  
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QY 388 ATGCAAGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 447  
Db 544 ATGCAAGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 603  
QY 448 AATCTACTATGCGCAAGAGCAATCTGTTCTCCCTTCCAGAGTCTCTCTGATTTAA 507  
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OM nucleic - nucleic search, using sw model

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Perfect score: 638

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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_bt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_mu.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rdt.\*

36: em\_htg\_rdt.\*

37: em\_htg\_vit.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result \* Query

No.	Score	Match	Length	DB	ID	Description
1	485	76.0	638	6	102042	102042 Sequence 5
2	485	76.0	638	6	108496	108496 Sequence 7
3	485	76.0	638	9	HUMCEGFB	M13361 Human beta-
4	434	68.0	638	6	108090	108090 Sequence 4
5	434	68.0	638	6	109138	109138 Sequence 3
6	434	68.0	1073	9	BC032697	BC032697 Homo sapi
7	434	68.0	2259	9	HSHEGFI	X51943 Human mRNA
8	418	65.5	490	6	AR380845	AR380845 Sequence
9	418	65.5	490	9	HSAGFG	X65778 H.sapiens a
10	408	63.9	464	9	S67291	S67291 Homo sapien
11	408	63.9	468	6	AR428605	AR428605 Sequence
12	408	63.9	468	6	AX481449	AX481449 Sequence 1
13	408	63.9	8501	6	A49428	A49428 Sequence 1
14	359	56.3	481	6	108499	108499 Sequence 13
15	359	56.3	481	6	109297	109297 Sequence 10
16	345	54.1	408	6	E37983	E37983 Process for
17	345	54.1	516	6	E26526	E26526 Sugar chain
18	345	54.1	525	6	E26510	E26510 Sugar chain
19	345	54.1	525	6	E37984	E37984 Process for
20	345	54.1	525	6	E37985	E37985 Process for
21	345	54.1	537	6	E38005	E38005 Process for
22	345	54.1	537	6	E38006	E38006 Process for
23	345	54.1	600	6	E26522	E26522 Sugar chain
24	345	54.1	600	6	E26523	E26523 Sugar chain
25	345	54.1	630	6	E26527	E26527 Sugar chain
26	345	54.1	663	6	E26509	E26509 Sugar chain
27	345	54.1	762	6	E26524	E26524 Sugar chain
28	345	54.1	843	6	E26525	E26525 Sugar chain
29	258	40.4	540	6	E26528	E26528 Sugar chain
30	255	40.0	543	6	E26511	E26511 Sugar chain
31	254	39.8	540	6	E38003	E38003 Process for
32	253	39.7	540	6	E38007	E38007 Process for
33	241	37.8	540	6	E38002	E38002 Process for
34	206	32.3	363	6	AX908985	AX908985 Sequence
35	206	32.3	363	6	BD044518	BD044518 Sequence
36	203	31.8	540	6	E38004	E38004 Process for
37	202	31.7	249	9	HUMFGFAB	L01487 Homo sapien
38	195	30.6	503	9	HUMFGFAL	M30490 Human acid
39	195	30.6	1082	9	HUMHGF1	M23017 Human hepar
40	195	30.6	76416	9	AC005370	AC005370 Homo sapi
C 41	195	30.6	89837	2	AC091822	AC091822 Homo sapi
C 42	195	30.6	146437	9	AC010489	AC010489 Homo sapi
C 43	195	30.6	191734	2	AC016560	AC016560 Homo sapi
C 44	186	29.2	454	6	A00069	A00069 Artificial
C 45	186	29.2	454	6	A00070	A00070 Artificial

# ALIGNMENTS

RESULT 1	102042	Sequence 5 from Patent US 4868113.	638 bp ss-DNA	linear	PAT 21-MAY-1993
LOCUS	102042	Sequence 5 from Patent US 4868113.	638 bp ss-DNA	linear	PAT 21-MAY-1993
DEFINITION	102042	Sequence 5 from Patent US 4868113.	638 bp ss-DNA	linear	PAT 21-MAY-1993
ACCESSION	102042	Sequence 5 from Patent US 4868113.	638 bp ss-DNA	linear	PAT 21-MAY-1993
VERSION	102042.1	GI:270417	638 bp ss-DNA	linear	PAT 21-MAY-1993
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 638)				
AUTHORS	Jaye,M., Burgess,W., Maciag,T. and Drohan,W.				
TITLE	Recombinant DNA vector encoding human endothelial cell growth factor				
JOURNAL	Patent: US 4868113-A 5 19-SEP-1989;				
FEATURES	Rorer Biotechnology, Inc.; King of Prussia, PA				
source	Location/Qualifiers				
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ORIGIN					
Query Match	76.0%; Score 485; DB 6; Length 638;				
Best Local Similarity	99.5%; Pred.No. 1.2e-250;				
Matches	635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
OY	1 GAATTCGGGAACGCCACAGCAGCAGCTGCTGAGCCATCGCTGAAGGGGAATCAACA 60				

Db 1 GAATTCGGGAACCGCCACCAAGCAGCAGCTGCTGAGCCATGCTGAGGGGAATCACA 60
Qy 61 CTTTCAGAGCCCTGACGAGAGGATTTAATCTGCTCAGGGAATTAAGAGAGCCCAAC 120
Db 61 CTTTCAGAGCCCTGACGAGAGGATTTAATCTGCTCAGGGAATTAAGAGAGCCCAAC 120
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LOCUS I08496
DEFINITION Sequence 7 from Patent WO 8701728.
ACCESSION I08496
VERSION I08496.1 GI:588798
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 638)
AUTHORS Fiddes, J.C. and Abraham, J.A.
TITLE RECOMBINANT FIBROBLAST GROWTH FACTORS
JOURNAL Patent: WO 8701728-A 7 26-MAR-1987;
FEATURES
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/mol\_type="unassigned DNA"
ORIGIN
Query Match 76.0%; Score 485; DB 6; Length 638;
Best Local Similarity 99.5%; Pred. No. 1.2e-250;
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GAATTCGGGAACCGCCACCAAGCAGCAGCTGCTGAGCCATGCTGAGGGGAATCACA 60
Db 1 GAATTCGGGAACCGCCACCAAGCAGCAGCTGCTGAGCCATGCTGAGGGGAATCACA 60
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Qy 121 TCCTCTACTGTAGCAACGGGGCCACTTTCCTGAGGATCCTTCGGGATGCGACAGTGGATG 180
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Qy 181 GGAAGAGGACAGAGGACGACACATTCAGCTGCACTGCGGAAAGGCTGGGGG 240
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Db 601 AACCCCGAGCCACAGAGCTGCAATTTGTAAGCACTT 638
RESULT 3
LOCUS HUMECGFB
DEFINITION Human beta-endothelial cell growth factor (ECGF-beta), mRNA, complete cds.
ACCESSION M13361
VERSION M13361.1 GI:181941
KEYWORDS endothelial cell growth factor-beta; growth factor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 638)
AUTHORS Jaye, M., Howk, R., Burgess, W., Ricca, G.A., Chiu, I.M., Ravera, M.W., O'Brien, S.J., Modi, W.S., Maciag, T. and Drohan, W.N.
TITLE Human endothelial cell growth factor: cloning, nucleotide sequence, and chromosome localization
JOURNAL Science 233 (4763), 541-545 (1986)
MEDLINE 86361805
PUBMED 3523756
COMMENT Original source text: Homo sapiens (clone: ECGF[1.29]) brain stem CDNA to mRNA.
Draft entry and clean copy sequence for [1] kindly provided by M.C. Jaye, 10-OCT-1986.
The beta-, and alpha-endothelial cell growth factor mRNAs and the aEGF-1 mRNA are probably transcribed from the same gene.
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Query Match 76.0%; Score 485; DB 9; Length 638;

Best Local Similarity 99.5%; Pred. No. 1.2e-250;  
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTCGGGAAAGCGGCGACACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAATTCACCA 60  
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QY 121 TCCCTACTGTAAGCAAGCGGGGCGACTTCTGAGGATCTCTCCGATGGGACAGTGATG 180  
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Db 601 AACCCGAGCAGCAGGCTGAAATTTGTAAGCACTT 638

RESULT 4  
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LOCUS 108090  
DEFINITION Sequence 4 from Patent EP 0298723.  
ACCESSION 108090  
VERSION 108090.1 GI:589198  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 638)  
AUTHORS Fiddes, J.C., Abraham, J.A. and Protter, A.  
TITLE Recombinant fibroblast growth factors  
JOURNAL Patent: EP 0298723-A1 4 11-JAN-1989;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

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Query Match 68.0%; Score 434; DB 6; Length 638;  
Best Local Similarity 100.0%; Pred. No. 4.8e-223;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 133 GCACACGGGGGCGACTTCTGAGGATCTTCCGGATGCGACAGTGGGCAAGGGGACA 192  
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LOCUS 109138  
DEFINITION Sequence 3 from Patent WO 8900198.  
ACCESSION 109138  
VERSION 109138.1 GI:588154  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 638)  
AUTHORS Fiddes, J.C., Abraham, J.A. and Protter, A.  
JOURNAL Patent: WO 8900198-A 3 12-JAN-1989;  
FEATURES Location/Qualifiers  
source 1..638  
/organism="unknown"  
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ORIGIN  
Query Match 68.0%; Score 434; DB 6; Length 638;  
Best Local Similarity 100.0%; Pred. No. 4.8e-223;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGCACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAATTCACCACTTCACAGCCC 72  
Db 65 GCGCACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAATTCACCACTTCACAGCCC 124

QY 73 TGACCGAGAGTTTAAATCTGCTCCAGGGAATTAACAAGAGCCCAACCTCTCTACTGTA 132  
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QY 133 GCACACGGGGGCGACTTCTGAGGATCTTCCGGATGCGACAGTGGGCAAGGGGACA 192  
Db 185 GCACACGGGGGCGACTTCTGAGGATCTTCCGGATGCGACAGTGGGCAAGGGGACA 244

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QY 373 ATATATCCAAGAGCATGCGAGAGAAATGGTTTGTGGCTTCAAGAAGATGGAGCT 432  
Db 425 ATATATCCAAGAGCATGCGAGAGAAATGGTTTGTGGCTTCAAGAAGATGGAGCT 484

QY 433 GCACACGGGCTCT 446  
Db 485 GCACACGGGCTCT 498

Db 485 GCMAACCGCGTCT 498

RESULT 6

BC032697

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

SOURCE

BC032697 1073 bp mRNA linear PRI 06-OCT-2003  
Homo sapiens fibroblast growth factor 1 (acidic), mRNA (cDNA clone  
MGC:44867 IMAGE:5403677), complete cds.

BC032697

BC032697.1 GI:21595686

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1073)

Strausberg, R.L., Feingold, R.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, P.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diachenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Hale, S., Garcia, A.M., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hales, S., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahy, J., Helton, E., Kettner, M., Madan, A., Young, A.C., Shevchenko, Y.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M.,

Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalios, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1073)

Strausberg, R.

Direct Submission

Submitted (06-JUN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)

Akhter, N., Ayele, K., Beckett, Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietch, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Madore, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>

Series: IRAC Plate: 69 Row: d Column: 4

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 15055546.

Location/Qualifiers

1. 1073

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="MGC:44867 IMAGE:5403677"

/tissue\_type="Liver, adenocarcinoma"

/clone\_lib="NIH\_MGC\_90"

/lab\_host="DHL08"

/notes="Vector: pCMV-SPORT6"

1. 1073

/gene="FGF1"

/notes="SYNonyms: FGFA, AFGE, ECGF, ECGFA, ECGFB, HBGFI,

ECGF-beta, FGF-alpha, GLI0703"

/db\_xref="LocusID:2246"

/db\_xref="MIM:113120"

91. 558

/codon\_start=1

/product="FGF1 protein"

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/db\_xref="LocusID:2246"

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157. 543

/notes="FCF, Region: Fibroblast growth factor. Fibroblast

growth factors are a family of proteins involved in growth

and differentiation in a wide range of contexts. These

growth factors cause dimerisation of their tyrosine kinase

receptors leading to intracellular signaling. There are

currently four known tyrosine kinase receptors for

fibroblast growth factors. These receptors can each bind

several different members of this family. Members of this

family have a beta trefoil structure"

/db\_xref="CDD:pfam00167"

Query Match 68.0%; Score 434; DB 9; Length 1073;

Best Local Similarity 100.0%; Pred. No. 4.6e-223;

Matches 434; Conservative 0; Mismatches 0; Gaps 0;

QY 13 GCGCCACACAGCAGCAGCTGCTGAGCCATGCTGAAAGGGAAATACACACCTTCACAGCC 72

Db 65 GCGCCACACAGCAGCAGCTGCTGAGCCATGCTGAAAGGGAAATACACACCTTCACAGCC 124

QY 73 TCACCGAGAGATTTTATCTGCTTCAGGGGAATTCAGAGCCCAAACTCTCTACTGTA 132

Db 125 TCACCGAGAGATTTTATCTGCTTCAGGGGAATTCAGAGCCCAAACTCTCTACTGTA 184

QY 133 GCACGCGGGGCGACCTTCCTGAGGATCTTCGCGATGCGACAGTGATGGGCAAGGACA 192

Db 185 GCACGCGGGGCGACCTTCCTGAGGATCTTCGCGATGCGACAGTGATGGGCAAGGACA 244

QY 193 GCAGCGACACAGCAGCAGCTGCTGAGCCATGCTGAAAGGGAAATTCAGAGCCCAAACTCTCTACTGTA 252

Db 245 GCAGCGACACAGCAGCAGCTGCTGAGCCATGCTGAAAGGGAAATTCAGAGCCCAAACTCTCTACTGTA 304

QY 253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGCGACCGCGGCTTTTATACGGCTCAC 312

Db 305 AGAGTACCGAGACTGGCCAGTACTTGGCCATGCGACCGCGGCTTTTATACGGCTCAC 364

QY 313 AGACACCAAAATGAGGAATTTTGTCTCGAAAGGCTGGAGAGACCACTTACACACCT 372

Db 365 AGACACCAAAATGAGGAATTTTGTCTCGAAAGGCTGGAGAGACCACTTACACACCT 424

QY 373 ATATATCCCAAGACATGCGAGAGAAATTTGTTGCTTCAGAGAGATGGAGCT 432

Db 425 ATATATCCCAAGACATGCGAGAGAAATTTGTTGCTTCAGAGAGATGGAGCT 484

QY 433 GCACGCGGGGCGACCTTCCTGAGGATCTTCGCGATGCGACAGTGATGGGCAAGGACA 446

Db 485 GCACGCGGGGCGACCTTCCTGAGGATCTTCGCGATGCGACAGTGATGGGCAAGGACA 498

RESULT 7

HSHPGF1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human mRNA for human heparin-binding growth factor 1/ acidic

fibroblast growth factor.

HSHPGF1 2259 bp mRNA linear PRI 12-SEP-1993

X51943

GI:32435

fibroblast growth factor; growth factor; heparin-binding growth

factor.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 2259)  
AUTHORS Chiu, I.-M., Wang, W. P. and Lehtoma, K.  
TITLE Alternative splicing generates two forms of mRNA coding for human heparin-binding growth factor 1  
JOURNAL Oncogene 5 (5), 755-762 (1990)  
MEDLINE 90265618  
PUBMED 1693186  
REFERENCE 2 (bases 1 to 2259)  
AUTHORS Chiu, I.-M.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-1990) Chiu I.-M., Dept of Internal Medicine, Davis Medical Research Centre, The Ohio State University, 480 West 9th Ave, Columbus OH 43210, USA  
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Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="pHGF1.1, 1.2, 1.3, 1.4 and 1.5"  
/tissue\_type="brain stem"  
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35. .502  
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Best Local Similarity 100.0%; Pred. No. 4.3e-223;  
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QY 13 GGGCGCAAGCAGCAGCTCTGAGCCATGGCTGGAAGGGGAATCACCACCTTCACAGCCC 72  
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QY 73 TGACCGAGAGTTTATCTGCTCCAGGGAATACAGAGGCCCAACCTCTCTACTGTA 132  
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QY 133 GCAACGGGGGCCATCTCTGAGGATCTTCGGATGGCAGATGGATGGGACAGGACA 192  
Db 129 GCAACGGGGGCCATCTCTGAGGATCTTCGGATGGCAGATGGATGGGACAGGACA 188  
QY 193 GGAGCCACGACGACATTCAGCTGACGCTCAGTGGGAGAGCGTGGGAGAGTGATATTA 252  
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QY 253 AGATACCTGAGATGGCCAGTACTTGGCCATGGACACCGAGCGGCTTTTATAGCGCTAC 312  
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QY 313 AGACACCAATAGGAGATGTTCTGCTGGAAAGCTGGAGAGACCAATTCACACCT 372  
Db 309 AGACACCAATAGGAGATGTTCTGCTGGAAAGCTGGAGAGACCAATTCACACCT 368  
QY 373 ATATATCCAGAGCATCCAGAGAGATTTGGTTTGGCTTCAAGAGAGATGGAGCT 432  
Db 369 ATATATCCAGAGCATCCAGAGAGATTTGGTTTGGCTTCAAGAGAGATGGAGCT 428  
QY 433 GCAACGGGGTCT 445  
Db 429 GCAACGGGGTCT 442

RESULT 8  
AR380845

LOCUS AR380845 490 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1390 from patent US 6607879.  
ACCESSION AR380845  
VERSION AR380845.1 GI:40088479  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 490)  
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.  
TITLE Compositions for the detection of blood cell and immunological response gene expression  
JOURNAL Patent: US 6607879-A 1390 19-AUG-2003;  
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source  
1. .490  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

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Query Match 65.5%; Score 418; DB 6; Length 490;  
Best Local Similarity 100.0%; Pred. No. 2.2e-214;  
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 29 CTGTGAGCCATGGCTGAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAA 88  
Db 1 CTGTGAGCCATGGCTGAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAA 60  
QY 89 TCTGCTCCAGGGAATTACAGAGCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 148  
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QY 149 CTGTGAGATCTTCCGATGGCAGAGTGGATGGGACAGGAGCAGAGCAGCAGACAT 208  
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QY 389 TGCAGAGAAGATTTGTTTGTGGCCCTCAAGAGAATGGAGCTGCMAACGGGCTCT 446  
Db 361 TGCAGAGAAGATTTGTTTGTGGCCCTCAAGAGAATGGAGCTGCMAACGGGCTCT 418

RESULT 9  
HSAFPG HSAFPG H.sapiens afGF mRNA for acidic fibroblast growth factor.  
ACCESSION X65778  
VERSION X65778.1 GI:396163  
KEYWORDS fibroblast growth factor; fibroblast growth factor acidic.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Yu, Y.L., Kha, H., Golden, J.A., Migheli, A.A., Goetzl, E.J. and Turk, C.W.  
TITLE An acidic fibroblast growth factor protein generated by alternate splicing acts like an antagonist  
JOURNAL J. Exp. Med. 175 (4), 1073-1080 (1992)  
MEDLINE 92202857  
PUBMED 1372643  
FEATURES  
source  
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Location/Qualifiers  
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ORIGIN

Query Match 65.9%; Score 418; DB 9; Length 490;  
Best Local Similarity 100.0%; Pred. No. 2.2e-214;  
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 29 CTCTGAGCCTGGCTGAAGGGGAATCACACCTTCACAGCCCTGACCGAGAGTTAA 88  
Db 1 CTCTGAGCCTGGCTGAAGGGGAATCACACCTTCACAGCCCTGACCGAGAGTTAA 60  
QY 89 TCTGCTCCAGAGGAATACAGAGCCCAACTCTCTACTGTAGCAACGGGGCCACTT 148  
Db 61 TCTGCTCCAGAGGAATACAGAGCCCAACTCTCTACTGTAGCAACGGGGCCACTT 120  
QY 149 CTGAGAGTCTTCCGATGGCAGTGGATGGGCAAGGGACAGGAGCCGACACAT 208  
Db 121 CTGAGAGTCTTCCGATGGCAGTGGATGGGCAAGGGACAGGAGCCGACACAT 180  
QY 209 TCAGTGCAGCTCAGTGGGAAGGCTGGGGGAGGTGTATTAAGAGTACGAGACTGG 268  
Db 181 TCAGTGCAGCTCAGTGGGAAGGCTGGGGGAGGTGTATTAAGAGTACGAGACTGG 240  
QY 269 CAGTACTTGGCCATGACACCGACGGCTTTTATACGGCTCAGACACCAAAATGAGGA 328  
Db 241 CAGTACTTGGCCATGACACCGACGGCTTTTATACGGCTCAGACACCAAAATGAGGA 300  
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Db 301 ATGTTTGTCTCGAAGGCTGGAGAGAACCAATCAACACTATATATCCAGAGCA 360  
QY 389 TCAGAGAGAAATGTTTGTGTGGCTCAAGAGAAATGGGAGCTGCAAAAGGGTCT 446  
Db 361 TCAGAGAGAAATGTTTGTGTGGCTCAAGAGAAATGGGAGCTGCAAAAGGGTCT 418

RESULT 10

S67291  
LOCUS S67291 464 bp mRNA linear PRI 06-MAR-2001  
DEFINITION Homo sapiens acidic fibroblast growth factor (aFGF) mRNA, partial cds.  
ACCESSION S67291  
VERSION S67291.1 GI:456823  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Zhao X.M., Yeoh T.K., Hiebert M., Frist W.H. and Miller G.G.  
The expression of acidic fibroblast growth factor (heparin-binding growth factor-1) and cytokine genes in human cardiac allografts and T cells  
JOURNAL Transplantation 56 (5), 1177-1182 (1993)  
MEDLINE 94069734  
PUBMED 7504343  
REMARK GenBank staff at the National Library of Medicine created this entry (NCBI gi396164070) from the original journal article.  
This sequence comes from Fig. 2A.

FEATURES

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1..464  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cardiac allograft"  
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ORIGIN

Query Match 63.9%; Score 408; DB 9; Length 464;  
Best Local Similarity 100.0%; Pred. No. 5.7e-209;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAATCACACCTTCACAGCCCTGACCGAGAGTTAAATCTGCCTCA 98  
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QY 99 GGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTCTGAGGATC 158  
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QY 159 CTTCGGATGGCAGTGGATGGGACAGGAGCAGGAGCCAGCAGCAATTCAGCTGCAG 218  
Db 121 CTTCGGATGGCAGTGGATGGGACAGGAGCAGGAGCCAGCAGCAATTCAGCTGCAG 180  
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QY 279 GCCATGACACCGACGGCTTTTATACGGCTCAGACACCAAAATGAGCAATCTTGTTC 338  
Db 241 GCCATGACACCGACGGCTTTTATACGGCTCAGACACCAAAATGAGCAATCTTGTTC 300  
QY 339 CTGGAAGGCTGGAGGAGAACCAATTAACAACCTATATATCAAGAGCATGCAGAGAG 398  
Db 301 CTGGAAGGCTGGAGGAGAACCAATTAACAACCTATATATCAAGAGCATGCAGAGAG 360  
QY 399 AATCTGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAAGGGTCT 446  
Db 361 AATCTGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAAGGGTCT 408

RESULT 11

AR428605  
LOCUS AR428605 468 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 3 from patent US 6642026.  
ACCESSION AR428605  
VERSION AR428605.1 GI:40188276  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 468)  
AUTHORS Stegmann, T.J., Kordyum, V.A., Slavchenko, I.Yu., Chernykh, S.I. and Vozianov, O.P.  
TITLE Method of producing biologically active human acidic fibroblast growth factor and its use in promoting angiogenesis  
JOURNAL Patent: US 6642026-A 3 04-NOV-2003;  
FEATURES  
1..468  
Location/Qualifiers  
/organism="unknown"  
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ORIGIN

Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 5.7e-209;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAATCACACCTTCACAGCCCTGACCGAGAGTTAAATCTGCCTCA 98  
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QY 99 GGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTCTGAGGATC 158  
Db 61 GGGAAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTCTGAGGATC 120  
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Db 361 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCCT 408  
RESULT 12  
AX481449  
LOCUS AX481449 468 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 63 from Patent WO02055693.  
ACCESSION AX481449  
VERSION AX481449.1 GI:22316363  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1  
AUTHORS Kreutzer R., Limmer S., Rost S. and Hadwiger P.  
TITLE Method for inhibiting the expression of a target gene  
JOURNAL Patent: WO 02055693-A 63 18-JUL-2002;  
Ribopharma AG (DE)  
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source Location/Qualifiers  
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Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 5.7e-209;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
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QY 219 CTAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCATTCAGCTGCAG 278  
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Db 301 CTGGAAGGCTGGAGAGACCAATTACCAACCTATATATCAAGAGCATGCAGAGAAG 360  
QY 399 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCCT 446  
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RESULT 13  
A49428  
LOCUS A49428 8501 bp DNA circular PAT 07-MAR-1997  
DEFINITION Sequence 1 from Patent WO9608572.  
ACCESSION A49428  
VERSION A49428.1 GI:2302907  
KEYWORDS

SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 8501)  
AUTHORS Cameron, B. and Crouzet, J.  
TITLE METHOD FOR THE PRODUCTION OF RECOMBINANT PROTEINS, PLASMIDS AND MODIFIED CELLS  
JOURNAL Patent: WO 9608572-A 1 21-MAR-1996;  
RHONE-POULENC RORER SA (FR)  
COMMENT Other publication AU 3475495 960329  
Other publication FR 2724665 960322.  
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ORIGIN  
Query Match 63.9%; Score 408; DB 6; Length 8501;  
Best Local Similarity 100.0%; Pred. No. 4.5e-209;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
Db 108 ATGGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 167  
QY 99 GGAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGCGGCGCCACTTCTCAGAGTC 158  
Db 168 GGAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGCGGCGCCACTTCTCAGAGTC 227  
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QY 399 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCCT 446  
Db 468 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCCT 515  
RESULT 14  
I08499  
LOCUS I08499 481 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 13 from Patent WO 8701728.  
ACCESSION I08499  
VERSION I08499.1 GI:588791  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 481)  
AUTHORS Fiddes, J.C. and Abraham, J.A.  
TITLE RECOMBINANT FIBROBLAST GROWTH FACTORS  
JOURNAL Patent: WO 8701728-A 13 26-MAR-1987;  
FEATURES  
source Location/Qualifiers  
1..481  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 56.3%; Score 359; DB 6; Length 481;  
Best Local Similarity 99.8%; Pred. No. 1.9e-182;  
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 37 CCAATGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCC 96  
Db 1 CCAATGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCC 60

```

Search completed: August 24, 2004, 22:17:43
Job time : 4178 secs

                                GenCore version 5.1.6
                                Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      August 24, 2004, 19:11:51 ; Search time 440 Seconds
              (without alignments)
              6159.887 Million cell updates/sec

Title:        US-10-022-554A-3
Perfect score: 638
Sequence:     1 gaattcggaacgcgcaca.....ccrگاatttgaagcaactt 638

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched:    3373863 seqs, 2124099041 residues

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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: Geneseqn2000s:*
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8: Geneseqn2003bs:*
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10: Geneseqn2004s:*

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score not as the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	1	638	100.0	638	8	ACAF04029		Actf04029 Thrombin
2	2	485	76.0	638	1	AAN70788		Aan70788 Complete
3	3	485	76.0	638	2	AAT37503		Aat37503 Human bet
4	4	485	76.0	638	2	AAX34350		Aax34350 Human end
5	5	485	76.0	638	8	AAX01723		Aax01723 Human end
6	6	485	76.0	638	8	ACF04028		Actf04028 Thrombin
7	7	444	69.6	639	2	AAC45985		Aac45985 Human end
8	8	434	68.0	638	1	AAN93088		Aan93088 Acidic fi
9	9	434	68.0	2357	9	ACC42968		Acc42968 Human Fib
10	10	434	68.0	4087	7	ABX63325		Abx63325 Human CDW
11	11	408	63.9	468	7	ABV78179		Abv78179 Human DNA
12	12	408	63.9	468	6	ABZ35755		Abz35755 Human pol
13	13	408	63.9	468	6	ABX09998		Abx09998 Human DNA
14	14	408	63.9	468	6	ABX98918		Abx98918 Human aci
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17	17	405	63.5	462	2	AAT45983		Aat45983 Human exp
18	18	359	56.3	481	1	AAN71029		Aan71029 Sequence
19	19	359	56.3	481	1	AAN90994		Aan90994 Partially
20	20	345	54.1	408	3	ACC66107		Acc66107 Human FGF
21	21	345	54.1	408	9	ADD68672		Add68672 Human DNA
22	22	345	54.1	434	9	ADD68674		Add68674 Human DNA
23	23	345	54.1	516	2	AAX81395		Aax81395 Polynucle
24	24	345	54.1	525	2	AAN81379		Aan81379 Polynucle
25	25	345	54.1	526	2	AAC63029		Aac63029 Polynucle

[illegible]



27 345 54.1 537 3 AAC66128 Mutant FG  
28 345 54.1 537 3 AAC66129 Mutant FG  
29 345 54.1 546 9 ADD68675 DNA ampli  
30 345 54.1 546 9 ADD68676  
31 345 54.1 600 2 AAX81392  
32 345 54.1 600 2 AAX81391  
33 345 54.1 602 9 ADD68692  
34 345 54.1 630 2 AAX81396  
35 345 54.1 647 9 ADD68691  
36 345 54.1 663 2 AAX81378  
37 345 54.1 707 9 ADD68686  
38 345 54.1 707 9 ADD68690  
39 345 54.1 762 2 AAX81393  
40 345 54.1 843 2 AAX81394  
41 309 48.4 405 2 AAT45984  
42 258 40.4 540 2 AAX81397  
43 255 40.0 543 2 AAX81380  
44 254 39.8 540 3 AAC66126  
45 253 39.7 540 3 AAC66130

#### ALIGNMENTS

RESULT 1  
ACF04029  
ID ACF04029 standard; DNA; 638 BP.  
XX AC ACF04029;  
XX XX  
DT 15-OCT-2003 (first entry)  
XX XX  
XX Thrombin resistant FGF-1 mutant coding sequence.  
XX XX  
XX Thrombin resistant FGF-1; FGF-1; fibroblast growth factor-1;  
KW myocardial ischaemia; peripheral vascular disease; cerebral ischaemia;  
KW epithelial injury; epidermal wound injury; nerve injury; mutant;  
KW bone damage; vasoprotective; cardiatic; cerebroprotective; vulnerary;  
KW neuroprotective; osteopathic; gene; ds.  
XX XX  
XX Homo sapiens.  
OS Synthetic.  
XX XX  
FH Key Location/Qualifiers  
FT CDS 42..506  
FT /tag= a  
FT /product= "FGF-1 mutant"  
FT /partial  
FT /note= "no start codon"  
XX W02003052378-A2.  
XX  
PD 26-JUN-2003.  
XX  
PF 11-DEC-2002; 2002WO-US039686.  
XX  
PR 17-DEC-2001; 2001US-00022554.  
XX  
PA (REPA-) REPAIR INC.  
PA (MAIN-) MAINE MEDICAL CENT RES INST.  
XX  
PI Maciag T, Ettenson DS, Burgess WH, Drohan WN;  
XX  
XX WPI; 2003-559052/52.  
DR P-PSDB; ABR63869.  
XX  
XX New thrombin degradation resistant fibroblast growth factor-1 (FGF-1)  
PT polypeptide, useful for treating a disease or disorder, e.g. cerebral  
PT ischaemia or bone damage, or for enhancing the effectiveness of an FGF-1  
PT response in a mammal.  
XX  
XX Claim 1; Fig 10; 83pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human  
CC fibroblast growth factor-1 (FGF-1) and a mutant that is resistant to  
CC thrombin degradation. The thrombin degradation resistant FGF-1 protein  
CC can be used for treating a disease or disorder (e.g. myocardial  
CC ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial  
CC injury, epidermal wound injury, nerve injury, or bone damage), for

CC enhancing the effectiveness of an FGF-1 response, or for stimulating an  
CC FGF-1 response in a mammal. The present sequence is the mutant FGF-1  
CC coding sequence  
XX  
SQ Sequence 638 BP; 175 A; 164 C; 166 G; 133 T; 0 U; 0 Other;  
Query Match 100.0%; Score 638; DB 8; Length 638;  
Best Local Similarity 100.0%; Pred. No. 1.8e-304;  
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCGGGAACCGCCACCAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCCCA 60  
Db 1 GAATTCGGGAACCGCCACCAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCCCA 60  
QY 61 CTTTCACAGCCCTGACCCAGCAGCTTTAATCTGCTCCAGGGAATTAACAAGACCCCAAC 120  
Db 61 CTTTCACAGCCCTGACCCAGCAGCTTTAATCTGCTCCAGGGAATTAACAAGACCCCAAC 120  
QY 121 TCTCTACTGTAGCAACGGGGGCCACTTCTGTAGGATCTTCTGCGATGGCAGTGGATG 180  
Db 121 TCTCTACTGTAGCAACGGGGGCCACTTCTGTAGGATCTTCTGCGATGGCAGTGGATG 180  
QY 181 GGACAGGGGACAGGAGGACGACGACATTCAGTCGAGCTCAGTCGCGAAGCGTGGGG 240  
Db 181 GGACAGGGGACAGGAGGACGACGACATTCAGTCGAGCTCAGTCGCGAAGCGTGGGG 240  
QY 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGTCGCGAAGCGTGGGG 300  
Db 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGTCGCGAAGCGTGGGG 300  
QY 301 TATAGGCTCAGACACACCAATAGGAGATGTTTCTTCTGGAAGGCTGGAGGAGAAC 360  
Db 301 TATAGGCTCAGACACACCAATAGGAGATGTTTCTTCTGGAAGGCTGGAGGAGAAC 360  
QY 361 ATTACACACCTATATATCCAGAGCATGCGAGAGATGTTTGTGGCTTCAAGA 420  
Db 361 ATTACACACCTATATATCCAGAGCATGCGAGAGATGTTTGTGGCTTCAAGA 420  
QY 421 AGAATGGGAGCTGCAACCGCGTCTTAAACTCACTATGSCCAGAAACCAATCTTGTTC 480  
Db 421 AGAATGGGAGCTGCAACCGCGTCTTAAACTCACTATGSCCAGAAACCAATCTTGTTC 480  
QY 481 TCCCTCTGCGAGCTCTCTGTGATTAAGAGATCTGTCTGTGTGTGACACTCCAGAA 540  
Db 481 TCCCTCTGCGAGCTCTCTGTGATTAAGAGATCTGTCTGTGTGTGACACTCCAGAA 540  
QY 541 GTTTCGAGGGGTCCTACCTGTTGACCCCAAAAATGTTCCCTTGACCATGGCTGGCT 600  
Db 541 GTTTCGAGGGGTCCTACCTGTTGACCCCAAAAATGTTCCCTTGACCATGGCTGGCT 600  
QY 601 AACCCCGCCACACAGAGCTGAATTTGAGCAACTT 638  
Db 601 AACCCCGCCACACAGAGCTGAATTTGAGCAACTT 638

RESULT 2  
AAN70788  
ID AAN70788 standard; cDNA; 638 BP.  
XX AC AAN70788;  
XX XX  
DT 25-MAR-2003 (revised)  
DT 13-MAY-1991 (first entry)  
XX  
XX Complete cDNA sequence of human endothelial cell growth factor (ECGF).  
XX Endothelial cell regeneration, blood vessel regeneration; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 39..506  
FT /tag= a  
FT mat\_peptide 42..83  
FT /tag= b  
FT /product= "Beta ECGF"  
FT mat\_peptide 84..101  
FT /tag= c  
FT /product= "Acidic FGF"

mat\_peptide 102..506  
/\*tag= d  
/product= "Alpha ECGF"

W08705332-A.  
11-SEP-1987.  
02-MAR-1987; 87WO-US000425.  
03-MAR-1986; 86US-00835594.  
(MELO-) MELOY LAB INC.  
(RORE) RORER BIOTECHNOLOGY INC.  
Jaye M, Burgess W, Maciag T, Drohan W;  
WPI; 1987-264128/37.  
P-PSDB; AAP70482.  
Human endothelial cell growth factor - produced by recombinant DNA techniques, useful for wound healing.  
Example; Fig 8; 43pp; English.  
To screen the human brain stem cDNA library for clones contg. ECGF inserts, a specific oligonucleotide was designed. This oligonucleotide was based upon a partial AA sequence analysis of the amino terminus of ECGF (see AAP70480 and AAP70481). Fig 3c sets forth for comparison the AA sequence of cyanogen bromide-cleaved bovine alpha and beta ECGF (AAP70834). The two clones that were isolated, ECGF clones 1 and 29, were analysed in further detail. The nucleotide sequence of these clones and the AA sequence deduced from the nucleic acid sequence is shown in Fig 8 (see AAP70788 and AAP70482). (Updated on 25-MAR-2003 to correct PA field.)

Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
Query Match 76.0%; Score 485; DB 1; Length 638;  
Best Local Similarity 99.5%; Pred. No. 5.9e-229;  
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTCGGGAGCGGCTCCTGCTGAGCCAGCAGCAGCTGCTGAGCCAGTGGCTGAAGGGAAATCAACA 60  
Db 1 GAATTCGGGAGCGGCTCCTGCTGAGCCAGCAGCAGCTGCTGAGCCAGTGGCTGAAGGGAAATCAACA 60  
QY 61 CTTTCAGAGCCCTGACCGAGAGTTTAACTCTGCTCCAGGGAATTACAGAGGCCCAAC 120  
Db 61 CTTTCAGAGCCCTGACCGAGAGTTTAACTCTGCTCCAGGGAATTACAGAGGCCCAAC 120  
QY 121 TCTCTACTGTAGCAGCGGGCCACTTCTGAGATCTTCCGATGCGACAGTGATG 180  
Db 121 TCTCTACTGTAGCAGCGGGCCACTTCTGAGATCTTCCGATGCGACAGTGATG 180  
QY 181 GGACAGGGACAGGAGCAGCAGCAGCAGCAGCTGAGCTGAGCTGCGGAAAGCTGGGG 240  
Db 181 GGACAGGGACAGGAGCAGCAGCAGCAGCAGCTGAGCTGAGCTGCGGAAAGCTGGGG 240  
QY 241 AGGTGTATTAAGAGTACCGAGCTGCGGAGTCTTGCCATGCGACCGAGCGGCTTT 300  
Db 241 AGGTGTATTAAGAGTACCGAGCTGCGGAGTCTTGCCATGCGACCGAGCGGCTTT 300  
QY 301 TATACGGCTTCACAGACCAAAATGAGGAATGTTTCTCGAAGGCTGCGAGCAACC 360  
Db 301 TATACGGCTTCACAGACCAAAATGAGGAATGTTTCTCGAAGGCTGCGAGCAACC 360  
QY 361 ATTACAGACCTATATTCAGAGCAGTGCAGAGAGATGGTGTGGCTCAAGA 420  
Db 361 ATTACAGACCTATATTCAGAGCAGTGCAGAGAGATGGTGTGGCTCAAGA 420  
QY 421 AGAATGGAGCTGCAAAAGCGGCTCTAAACTCTATGTCGAGAGAGCATCTGTTTC 480  
Db 421 AGAATGGAGCTGCAAAAGCGGCTCTCGGACTCTATGTCGAGAGAGCATCTGTTTC 480  
QY 481 TCCCTGCTCCAGTCTCTTGTATTAAGAGATCTGTTGTGTTGAGCAGTCCAGAA 540  
Db 481 TCCCTGCTCCAGTCTCTTGTATTAAGAGATCTGTTGTGTTGAGCAGTCCAGAA 540  
QY 541 GTTTCGGGGTCTCCTGCTGTTGAGCCCAAAATGTTCCCTTGACCATTTGGCTGCGCT 600

Db 541 GTTTCGGGGTCTCCTGCTGTTGAGCCCAAAATGTTCCCTTGACCATTTGGCTGCGCT 600  
QY 601 AACCCCGAGCCACAGAGCTGTAATTTGAAGCAACTT 638  
Db 601 AACCCCGAGCCACAGAGCTGTAATTTGAAGCAACTT 638

RESULT 3  
AAT37503  
ID AAT37503 standard; DNA; 638 BP.  
XX  
AC AAT37503;  
XX  
DT 25-MAR-2003 (revised)  
DT 23-DEC-1996 (first entry)  
XX  
DE Human beta-endothelial cell growth factor.  
XX  
KW Endothelial cell growth factor; ECGF; blood vessel; regeneration;  
KW heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;  
XX fibroblast growth factor; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 39..506  
FT /\*tag= a  
FT misc\_RNA 42..503  
FT /\*tag= b  
FT /\*label= beta-ECGF  
FT misc\_RNA 84..503  
FT /\*tag= c  
FT /\*label= acidic\_FGF  
FT misc\_RNA 102..503  
FT /\*tag= d  
FT /\*label= alpha-ECGF  
XX  
US5552528-A.  
XX  
PD 03-SEP-1996.  
XX  
XX 03-NOV-1994; 94US-00334884.  
XX  
XX 03-MAR-1986; 86US-00835594.  
PR 18-DEC-1987; 87US-00334499.  
PR 29-APR-1991; 91US-00693079.  
PR 27-NOV-1991; 91US-00799859.  
XX  
(RHON) RHONE POULENC RORER PHARM INC.  
XX  
XX Maciag T, Burgess W;  
PI  
XX WPI; 1996-412132/41.  
DR F-PSDB; AAW04805, AAW04806, AAW04807.  
XX  
FT Isolated, purified, biologically active bovine beta endothelial cell growth factor - useful to regenerate or treat damaged blood vessels.  
XX  
PS Disclosure; Fig 8; 28pp; English.  
XX  
CC Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a mol.wt. of 20 KD can be purified at least 16300 fold from bovine brain using heparin-Sepharose affinity chromatography. ECGF is useful for, among other purposes, diagnostic applications and has potential in the treatment of damaged blood vessels or other endothelial cell-lined structures. Human ECGF (AAT37503) or fragments may be obtained using oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
XX

Query Match 76.0%; Score 485; DB 2; Length 638;  
Best Local Similarity 99.5%; Pred. No. 5.9e-229;  
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTCGGGAGCGGCTCCTGCTGAGCCAGCAGCAGCTGCTGAGCCAGTGGCTGAAGGGAAATCAACA 60  
|||||



KW regenerate; blood vessel; endothelial cell; human; ss.  
XX Homo sapiens.  
OS Key Location/Qualifiers  
XX CDS 39..506  
FT /\*tag= a  
FT /product= "ECGF"  
FT misc\_feature 42  
FT /\*tag= b  
FT /note= "beta-ECGF begins at this position"  
FT misc\_feature 84  
FT /\*tag= c  
FT /note= "acidic PGF begins at this position"  
FT misc\_feature 102  
FT /\*tag= d  
FT /note= "alpha-ECGF begins at this position"  
XX  
XX US5849538-A.  
XX 15-DEC-1998.  
XX  
XX 11-APR-1997; 97US-00840088.  
XX 03-MAR-1986; 86US-00835594.  
XX 18-DEC-1987; 87US-00134499.  
XX 29-APR-1991; 91US-00693079.  
XX 27-NOV-1991; 91US-00799859.  
XX 03-NOV-1994; 94US-00334884.  
XX 07-JUN-1995; 95US-00472964.  
XX 04-NOV-1996; 96US-00743261.  
XX  
XX (RHON ) RHONE-POULENC RORER PHARM INC.  
XX  
XX Jaye M, Burgess W, Maciag T, Drohan WN;  
XX WPI: 1999-069734/06.  
XX P-PSDB; AAW92291.  
XX  
XX DNA encoding a cleavable signal peptide and an endothelial cell growth factor - useful for producing recombinant endothelial cell growth factor proteins.  
XX  
XX Disclosure; Fig 8; 23pp; English.  
XX  
XX The invention relates to DNA encoding human endothelial cell growth factors (ECGF) and plasmids comprising the DNA sequences. The DNA encodes a cleavable signal peptide and an ECGF, where removal of the signal peptide yields a mature form of the ECGF, where the ECGF is alpha-ECGF or beta-ECGF. The DNA is used to produce recombinant ECGF proteins, which can be used in treatments to repair or regenerate blood vessels or other structures lined with endothelial cells. The present sequence represents a human ECGF cDNA sequence (determined from lambda ECGF clones 1 and 29)  
XX  
XX Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
SQ

Query Match 76.0%; Score 485; DB 2; Length 638;  
Best Local Similarity 99.5%; Pred. No. 5.9e-229;  
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GAATTCGGGAACGGCCCAAGCAGCAGCAGCTCTGAGCCATCGCTGAAGGGGAATCACC 60  
Db |||||||  
QY 1 GAATTCGGGAACGGCCCAAGCAGCAGCAGCTCTGAGCCATCGCTGAAGGGGAATCACC 60  
Db |||||||  
QY 61 CTTTCACAGCCCTGACCCAGAGAGTTTAAATCTGCTCCAGGGAATTACAGAGCCCAAC 120  
Db |||||||  
QY 121 TCCTCTACTGTAGCAACGGGGGCCACTTCTCGAGGATCTTTCGGATGGCAGATGATG 180  
Db |||||||  
QY 121 TCCTCTACTGTAGCAACGGGGGCCACTTCTCGAGGATCTTTCGGATGGCAGATGATG 180  
Db |||||||  
QY 181 GGACAGGAGCAGAGGAGCAGCAGCATTGAGCTGAGCTGAGTGGGGAAGCGTGGGG 240  
Db |||||||  
QY 181 GGACAGGAGCAGAGGAGCAGCAGCATTGAGCTGAGCTGAGTGGGGAAGCGTGGGG 240  
QY 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGAACACCGAGCGCTTT 300  
Db |||||||  
QY 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGAACACCGAGCGCTTT 300

QY 301 TATACGGCTCAGACACCAATGAGGAATGTTTGTTCCTGGAAGGCTCGAGGAGACC 360  
Db |||||||  
QY 301 TATACGGCTCAGACACCAATGAGGAATGTTTGTTCCTGGAAGGCTCGAGGAGACC 360  
Db |||||||  
QY 361 ATTACAAACCTATATATCCAGAGCAATCCAGAGCAATGTTGTTGCTCAGAA 420  
Db |||||||  
QY 361 ATTACAAACCTATATATCCAGAGCAATCCAGAGCAATGTTGTTGCTCAGAA 420  
Db |||||||  
QY 421 AGAATGGAGCTCAAAAGCGGCTCTAAACCTCATATGCGCAGAAAGCAATCTGTTTC 480  
Db |||||||  
QY 421 AGAATGGAGCTCAAAAGCGGCTCTCGGACTCACTATGCGCAGAAAGCAATCTGTTTC 480  
Db |||||||  
QY 481 TCCCTCTCCAGTCTCTCTGATTAAGAGATCTGTTGTTGTTGTTGTTGTTGTTTC 540  
Db |||||||  
QY 481 TCCCTCTCCAGTCTCTCTGATTAAGAGATCTGTTGTTGTTGTTGTTGTTGTTTC 540  
Db |||||||  
QY 541 GTTTCGAGGGGCTCCTACCTGTTGACCCCAAAAATGTTCCCTTGACCATGCTGCGCT 600  
Db |||||||  
QY 541 GTTTCGAGGGGCTCCTACCTGTTGACCCCAAAAATGTTCCCTTGACCATGCTGCGCT 600  
Db |||||||  
QY 601 AACCCCGAGCCACAGAGCCTGAAATTTGTAAGCACTT 638  
Db |||||||  
QY 601 AACCCCGAGCCACAGAGCCTGAAATTTGTAAGCACTT 638  
Db |||||||  
RESULT 6  
ID ACF04028 standard; DNA; 638 BP.  
XX ACF04028;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
XX Thrombin resistant FGF-1 mutant production wildtype coding sequence.  
XX  
XX Thrombin resistant FGF-1; FGF-1; fibroblast growth factor-1;  
XX myocardial ischaemia; peripheral vascular disease; cerebral ischaemia;  
XX epithelial injury; epidermal wound injury; nerve injury; bone damage;  
XX vasotropic; cardiant; cerebroprotective; vulnerary; neuroprotective;  
XX osteopathic; gene; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 42..506  
FT /\*tag= a  
FT /product= "FGF-1"  
FT /partial  
FT /note= "no start codon"  
XX  
XX WO2003052378-A2.  
XX  
XX 26-JUN-2003.  
XX  
XX 11-DEC-2002; 2002WO-US039686.  
XX  
XX 17-DEC-2001; 2001US-00022554.  
XX  
XX (REPA-) REPAIR INC.  
XX (MAIN-) MAINE MEDICAL CENT RES INST.  
XX  
XX Maciag T, Ettenson DS, Burgess WH, Drohan WN;  
XX  
XX WPI: 2003-559052/52.  
XX P-PSDB; ABR63868.  
XX  
XX New thrombin degradation resistant fibroblast growth factor-1 (FGF-1) polypeptide, useful for treating a disease or disorder, e.g. cerebral ischemia or bone damage, or for enhancing the effectiveness of an FGF-1 response in a mammal.  
XX  
XX Claim 2; Fig 8; 83pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human fibroblast growth factor-1 (FGF-1) and a mutant that is resistant to thrombin degradation. The thrombin degradation resistant FGF-1 protein can be used for treating a disease or disorder (e.g. myocardial ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial

\_\_\_\_\_

RESULT 8  
 AAN93088  
 ID AAN93088 standard; DNA; 638 BP.  
 XX AAN93088;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 25-JUN-1990 (first entry)  
 XX  
 DE Acidic fibroblast growth factor.  
 XX  
 KW Acidic fibroblast growth factor; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT mat\_peptide 91..555  
 FT /tag= a  
 FT /label= human acidic fibroblast growth factor  
 XX  
 FN EP298723-A.  
 XX  
 PD 11-JAN-1989.  
 XX  
 PF 06-JUL-1988; 88EP-00306158.  
 XX  
 PR 07-JUL-1987; 87US-00070797.  
 XX  
 PA (BIOU ) BIOTECH RES INST.  
 XX  
 PI Fides JC, Abraham JA, Protter A;  
 XX  
 DR WPI; 1989-009785/02.  
 DR N-PSDB; AAN93087.  
 XX  
 XX Recombinant DNA encoding new fibroblast growth factor analogues - useful  
 PT e.g. for accelerating wound healing and to control neovascularisation.  
 XX  
 PS Disclosure; Fig 2; 44pp; English.  
 XX  
 CC The sequence encodes human acidic fibroblast growth factor (aFGF). See  
 CC also AAN93087 and AAN93089. (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 638 BP; 170 A; 156 C; 168 G; 144 T; 0 U; 0 Other;  
 XX  
 Query Match 68.0%; Score 434; DB 1; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-204;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 GCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATACCAAGCCCAAACTCTCTACTGTA 72  
 Db 65 GCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATACCAAGCCCAAACTCTCTACTGTA 124  
 QY 73 TGACCCGAGAGCTTTAATCTGCTCCAGGGAATACCAAGCCCAAACTCTCTACTGTA 132  
 Db 125 TGACCCGAGAGCTTTAATCTGCTCCAGGGAATACCAAGCCCAAACTCTCTACTGTA 184  
 QY 133 GCAACGGGGCCACTTCTGAGGATCTTCCGGATGGCAGCAGTGGATGGGACAGGACA 192  
 Db 185 GCAACGGGGCCACTTCTGAGGATCTTCCGGATGGCAGCAGTGGATGGGACAGGACA 244  
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 Db 245 GGAGCCACGACATTCAGCTCAGCTCAGTCCGGAAGCGTGGGGAGGTGTATATA 304  
 QY 253 AGAGTACCGAGCTGGCCAGTCTGGCCATGGACCGAGGGCTTTTATACGGCTAC 312  
 Db 305 AGAGTACCGAGCTGGCCAGTCTGGCCATGGACCGAGGGCTTTTATACGGCTAC 364  
 QY 313 AGACACCAATAGGAATGTTTCTTGGAAAGCTGGAGAGCAACATACACACT 372  
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 QY 373 ATATATCCAGAGCATCCAGAGAGATTTGTTTGGCTCTAAGAGATGGAGCT 432  
 Db 425 ATATATCCAGAGCATCCAGAGAGATTTGTTTGGCTCTAAGAGATGGAGCT 484  
 QY 433 GCAACGGGTCTCT 446  
 |||||

Db 485 GCAACGGGTCTCT 498  
 RESULT 9  
 ACC42968  
 ID ACC42968 standard; DNA; 2357 BP.  
 XX ACC42968;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human Fibroblast Growth Factor 1 coding sequence.  
 XX  
 KW Human; Fibroblast Growth Factor 1; FGF1; acidic FGF; aFGF;  
 KW acidic Fibroblast Growth Factor; protein co-ordinate data; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 142..609  
 FT /tag= a  
 FT /product= "FGF1"  
 XX  
 FN WO2003038054-A2.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 31-OCT-2002; 2002WO-US034986.  
 XX  
 PR 31-OCT-2001; 2001US-0335583P.  
 XX  
 PA (UINY ) UNIV NEW YORK STATE.  
 XX  
 PI Moosa M, Green DL, Linhard RJ;  
 XX  
 DR WPI; 2003-482144/45.  
 DR P-PSDB; ABR56165.  
 XX  
 XX Composition useful for identifying modulators of fibroblast growth factor  
 PT -mediated signaling for use in treating cancer, has ternary complex of  
 PT FGF-receptor, FGF ligand and heparin agonist or antagonist.  
 XX  
 PS Disclosure; Fig 16B; 288pp; English.  
 XX  
 CC The present invention relates to an isolated composition comprising a  
 CC ternary complex of an Fibroblast Growth Factor (FGF) ligand polypeptide  
 CC (ABR56163, ABR56165), an FGF receptor polypeptide (ABR56164) and a  
 CC heparin agonist or antagonist, where the agonist or antagonist binds to  
 CC the FGF ligand polypeptide and the FGF receptor polypeptide to form the  
 CC ternary complex. The composition is useful for identifying a compound  
 CC that is an inhibitor of FGF receptor activity. FGF1 is also known as  
 CC acidic FGF  
 XX  
 SQ Sequence 2357 BP; 691 A; 521 C; 567 G; 578 T; 0 U; 0 Other;  
 XX  
 Query Match 68.0%; Score 434; DB 9; Length 2357;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-204;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 GCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATACCAAGCCCAAACTCTCTACTGTA 72  
 Db 116 GCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATACCAAGCCCAAACTCTCTACTGTA 175  
 QY 73 TGACCCGAGAGCTTTAATCTGCTCCAGGGAATACCAAGCCCAAACTCTCTACTGTA 132  
 Db 176 TGACCCGAGAGCTTTAATCTGCTCCAGGGAATACCAAGCCCAAACTCTCTACTGTA 235  
 QY 133 GCAACGGGGCCACTTCTGAGGATCTTCCGGATGGCAGCAGTGGATGGGACAGGACA 192  
 Db 236 GCAACGGGGCCACTTCTGAGGATCTTCCGGATGGCAGCAGTGGATGGGACAGGACA 295  
 QY 193 GGAGCCACGACATTCAGCTCAGCTCAGTCCGGAAGCGTGGGGAGGTGTATATA 252  
 Db 296 GGAGCCACGACATTCAGCTCAGCTCAGTCCGGAAGCGTGGGGAGGTGTATATA 355  
 QY 253 AGAGTACCGAGCTGGCCAGTCTGGCCATGGACCGAGGGCTTTTATACGGCTAC 312  
 Db 356 AGAGTACCGAGCTGGCCAGTCTGGCCATGGACCGAGGGCTTTTATACGGCTAC 415



XX The invention relates to inhibiting expression of a target gene (I) in a  
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded  
CC structure of at most 49 consecutive bases. At least part of one strand  
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA  
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
CC in humans, also genes in Plasmodium or in viruses or viroids that are  
CC pathogenic for humans, animals or plants. Introducing an overhang into  
CC dsRNA greatly increases effectiveness for inhibiting gene expression,  
CC both in vivo and in vitro and also increases stability and thus the  
CC effective concentration inside the cell. The present sequence is that of  
CC a gene related to the invention  
XX  
SQ Sequence 468 BP; 133 A; 115 C; 126 G; 96 T; 0 U; 0 Other;

Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 6e-191;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Qy 99 GGGAAATTACAGAGGCCCAACTCTCTACTGTGTAGCAACGGGGGGCCCTTCTCTGAGATC 158  
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Db 61 GGGAAATTACAGAGGCCCAACTCTCTACTGTGTAGCAACGGGGGGCCCTTCTCTGAGATC 120  
|||||

159 CTTCCGGATGGCACAAGTGGATGGGACAGGACAGGAGCAGCAGCAGCATTTTCAGCTGCAG 218  
|||||  
121 CTTCCGGATGGCACAAGTGGATGGGACAGGACAGGAGCAGCAGCAGCATTTTCAGCTGCAG 180

[illegible][illegible]

301 CTGGAAGGGCTGGAGGAGAACCAATTACAAACCTATATATCCAAAGACGATGCAGAGG 360

399 AATTGTGTTTGTGGGCTCAAGAGAATGGGAGCTGCAAAGCGGCTCT 446

361 AATTGTTTCTGGCTCAGACAGAAATGGGAGCTGCAAACGGCGTCTT 408

AB235755 standard; DNA; 468 bp.  
XX AC AB235755.

07-FEB-2003 (first entry)  
Human polynucleotide SEQ ID NO 63

Double stranded RNA; dsRNA; RNA inhibition; cytostatic; virucide; protozoicide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus.

Hepatitis C virus; human papilloma virus; gene; ds.  
Homo sapiens.

DEALING WITH THE  
18-JUL-2002.  
09-JUN-2001. 2001-06-09

09-JAN-2001; 2001DE-0100588.  
(RHO-) PRODRAPWA NC

X Kreutzer R, Limmer S, Rost S, Hadwiger P;  
X  
X  
R WPI: 2002-683450/74.

XX Inhibiting expression of target genes, useful e.g. for treating tumors,  
PT by introducing into cells two double-stranded RNAs that are complementary  
PT to the target.  
XX  
PS Claim 13; Page 44; 100pp; German.

The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRNAi and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAi and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNAi, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention

Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;

Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 6e-191;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 ATGGCTGAGGGGAAATCACCACTTTCAGCCCTGACGAGAGAGTTTAATCTGCTCCA 98  
|||||  
Db 1 ATGGCTGAGGGGAAATCACCACTTTCAGCCCTGACGAGAGAGTTTAATCTGCTCCA 60

QY 59 GGGAAATTACAGAGAGCCCAAACTCCTTACTGTAGCAAGGGGGCCACTTCTTGAGATC 158  
 |||||  
 Db 61 GGGAAATTACAGAGAGCCCAAACTCCTTACTGTAGCAAGGGGGCCACTTCTTGAGATC 120

139 CTTCGGATGACACAGTGGATGGGACAGGACAGCAGCACCAGCAGCATTTTCAGCTGGAG 218  
 |||||  
 121 CTTCGGATGGACAGTGGATGGGACAGGACAGCAGCAGCAGCAGCAGCATTCAGCTGGAG 180

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241 GCATGACACCGACGGGGCTTTTATACGGCTCCAGACACCAATGCGATGTTTGTC 300  
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301 CTGGAAAGCGTGGAGGAGAACCATTTCAACACCTATATATCCAAAGACGATCGCAGAGAAG 360

399 AATTGGTTTGTGGCGCTCAAGAAAGATGGGAGCTGCAAAGCGGCTCT 446

361 AATTGGTTTGTGGCTCAGAGAGATGGAGCTGCAACGGCTCT 408

ABX09998  
ID ABX09998 standard; DNA; 458 bp.  
XX  
AC ABX09998.

XX  
23-JAN-2003 (first entry)  
XX  
Human DNA fragment SRO ID 63  
DE

XX Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;  
 XV prion; inhibition; human; ds.  
 XX

DE10100587-Cl.  
Homo sapiens.  
DE10100587-Cl.  
Homo sapiens.

09-JAN-2001; 2001DE-01000587.

00 SAN 2002, 20042E-01000387.



PH	Key	Location/Qualifiers
FT	CDS	122..589
FT		/tag= a
FT		/product= "Protein of human acidic fibroblast growth factor (155AA)"
XX		
PN		WO200214468-A2.
PD		
PD		21-FEB-2002.
PF		15-AUG-2001; 2001WO-US025477.
XX		
PR		15-AUG-2000; 2000US-0225437P.
XX		
XX		(PHAG-) PHAGE BIOTECHNOLOGY CORP.
PI		Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;
XX		WPI; 2002-269184/31.
DR		P-PSDB; AAO19990.
XX		
FT		Bacteriophage-dependent method for producing biologically active proteins or peptides, involves employing an Escherichia coli transformed with a plasmid containing the targeted gene(s) operably linked to a promoter.
PT		
PT		Disclosure; Page 36-37; 44pp; English.
XX		
CC		The invention relates to a method for enhancing the production of a biologically active protein comprising infecting a strain of Escherichia coli, which has been transformed with a plasmid having at least one copy of an expressible gene, such as a human acidic fibroblast growth factor. The expressible gene encodes a biologically active protein operably linked to a phase T7 polymerase promoter, with a bacteriophage capable of mediating delayed lysis. The method is useful for the phage dependent superproduction of biologically active protein and peptides. The method is particularly useful for enhancing the production of heterologous proteins in bacterial host cells. This polynucleotide sequence represents the DNA of a human acidic fibroblast growth factor - FGF Ir HUMECSFB of the invention.
XX		
SQ		Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;
	Query Match	63.9%; Score 408; DB 6; Length 468;
	Best Local Similarity	100.0%; Pred. No. 6e-191;
	Matches 408; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	39	ATGCTGAAGGGGAATCACCACTTCTACAGCCCTCAGCGAAGTTTAATCTGCCTCCA 98
db		
QY	1	ATGCTGAAGGGGAATCACCACTTCTACAGCCCTCAGCGAAGTTTAATCTGCCTCCA 60
db		
QY	99	GCGAATTACAGAAGCCCAAACTCTCTACTGTAGCAGCGGGGCCACTTCTGAGATC 158
db		
QY	61	GCGAATTACAGAAGCCCAAACTCTCTACTGTAGCAGCGGGGCCACTTCTGAGATC 120
db		
QY	159	CTTCGGGANTGGCAAGTGGATGGATGGAGGACAGGACGACCAATTCAGCTGCAG 218
db		
QY	121	CTTCGGGANTGGCAAGTGGATGGAGGACAGGACGACCAATTCAGCTGCAG 180
db		
QY	219	CTCAGTCGGAAGCGTGGGGAGTGTATATAAGATGACCGAGCTGGCCAGTACTTG 278
db		
QY	181	CTCAGTCGGAAGCGTGGGGAGTGTATATAAGATGACCGAGCTGGCCAGTACTTG 240
db		
QY	279	GCCATGGACACCGAGGGCTTTTATACGGCTCAGACACACCAATGAGGAATGTTGTC 338
db		
QY	241	GCCATGGACACCGAGGGCTTTTATACGGCTCAGACACACCAATGAGGAATGTTGTC 300
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QY	339	CTGGAAAGGCTGGAGGAGACCAATTACACACTTATATCCAAAGACATGCAGAGAAG 398
db		
QY	301	CTGGAAAGGCTGGAGGAGACCAATTACACACTTATATATCCAAAGACATGCAGAGAAG 360
db		
QY	399	AATTGGTTTGTGGCCTCAAGAGAAGTGGAGCTGCACAGCGGTCT 446
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db		
RESULT 15		
BL91720		
ABL91720		standard; DNA: 468 BP.

AC ABL91720;  
XX 28-MAY-2002 (first entry)  
XX Human polynucleotide SEQ ID NO 63.  
XX  
XX Human; HIV; HCV; Gene expression; oligoribonucleotide; tumour; pathogen;  
KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;  
KW cytotatic; virucide; protozoacide; antibacterial; ds.  
XX Homo sapiens.  
XX DE10100586-C1.  
XX 11-APR-2002.  
XX 09-JAN-2001; 2001DE-01000586.  
XX 09-JAN-2001; 2001DE-01000586.  
XX (RIBO-) RIBOPHARMA AG.  
XX Kreutzer R, Linmer S, Rost S, Hadwiger P;  
XX WPI; 2002-270454/32.  
XX  
XX Inhibiting gene expression in cells, useful for e.g. treating tumors, by  
PT introducing double-stranded complementary oligorNA having unpaired  
PT terminal bases.  
XX  
XX Claim 13; Page 47; 104pp; German.  
XX  
XX The invention relates to a method for inhibiting expression of a target  
CC gene (ABL91658-ABL91797) in a cell by introducing at least one  
CC oligoribonucleotide that has a double-stranded structure consisting of at  
CC most 49 sequential nucleotide pairs, with at least part of one strand  
CC complementary with the target gene and has at least one end a single-  
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for  
CC antisense inhibition of gene expression useful e.g. for treating tumours  
CC but the oligoribonucleotides may also be directed against genes present  
CC in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,  
CC animals or plants) or against cytokine, Id, developmental or prion genes.  
CC The method provides more effective inhibition of gene expression than use  
CC of known oligonucleotides, probably because the unpaired overhang  
CC increases stability and thus intracellular concentration  
XX  
SQ Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;

Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 6e-191;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAAATACACCTTCAAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
Db |||||  
1 ATGGCTGAAGGGGAAATACACCTTCAAGCCCTGACCGAGAGTTTAACTGCTCCA 60  
QY 99 GCGAATTACAGAGCCCAACTCTCTACTGTAGCAAGCGGGGCCACTTCTGAGGATC 158  
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61 GGGAAATTACAGAGCCCAACTCTCTACTGTAGCAAGCGGGGCCACTTCTGAGGATC 120  
QY 159 CTCCTGGATGCGACAGTGGATGGGACAGGAGGACAGGACCACTTCACTGCGAG 218  
Db |||||  
121 CTCCTGGATGCGACAGTGGATGGGACAGGAGGACAGGACCACTTCACTGCGAG 180  
QY 219 CTCAGTGGGAAAGCGTGGGGGAGGTGTATTAAGAGTACCGAGTGGCGAGTCTGTC 278  
Db |||||  
181 CTGAGTGGGAAAGCGTGGGGGAGGTGTATTAAGAGTACCGAGTGGCGAGTCTGTC 240  
QY 279 GCGATGACACCGGCGCTTTTATACGGCTCTACAGACCAATGAGGATGTTTGTTC 338  
Db |||||  
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QY 339 CTGGAAGGCTGAGGAGACCAATACACCTTATATCCAGAGATGACAGAGAG 398  
Db |||||  
301 CTGGAAGGCTGAGGAGACCAATACACCTTATATCCAGAGATGACAGAGAG 360  
QY 399 AATTGGTGTGTTGGCTCTCAAGAGAAATGGGAGCTGCAACCGCTCT 446  
Db |||||  
361 AATTGGTGTGTTGGCTCTCAAGAGAAATGGGAGCTGCAACCGCTCT 408

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GenCore version 5.1.6  
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Perfect score: 638  
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Searched: 682709 seqs, 277475446 residues  
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Minimum DB seq length: 0  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES														
Result No.	Score	Query Match	Length	DB	ID	Description								
1	434	68.0	638	3	US-09-098-628-3	Sequence 3, Appli								
2	418	65.5	490	4	US-09-023-655-1390	Sequence 1390, Ap								
3	408	63.9	468	4	US-09-929-945-3	Sequence 3, Appli								
4	408	63.9	8501	3	US-08-793-900-1	Sequence 1, Appli								
5	186	29.2	454	6	5175147-1	Patent No. 5175147								
6	172	27.0	197	6	5514566-3	Patent No. 5514566								
7	118	18.5	450	6	5437995-1	Patent No. 5437995								
8	77	12.1	454	3	US-09-030-613-14	Sequence 14, Appl								
9	77	12.1	454	4	US-09-451-905-14	Sequence 14, Appl								
10	26	4.1	630	4	US-09-929-945-1	Sequence 1, Appli								
11	24	3.8	270	6	5514566-1	Patent No. 5514566								
12	23	3.6	44	1	US-08-023-757-8	Sequence 8, Appli								
13	23	3.6	44	1	US-08-177-502-8	Sequence 8, Appli								
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15	23	3.6	44	2	US-08-383-621-11	Sequence 2, Appli								
16	23	3.6	44	3	US-08-459-906-11	Sequence 11, Appl								
17	23	3.6	261	6	5514566-12	Patent No. 5514566								
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24	23	3.6	471	1	US-08-290-373B-15	Sequence 15, Appl								
25	23	3.6	477	1	US-08-290-373B-16	Sequence 16, Appl								
26	21	3.3	59	3	US-09-030-613-25	Sequence 25, Appl								
27	21	3.3	59	4	US-09-451-905-25	Sequence 25, Appl								
28	21	3.3	630	4	US-09-929-945-4	Sequence 4, Appli								
29	21	3.3	630	4	US-09-929-945-6	Sequence 6, Appli								

## ALIGNMENTS

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Best Local Similarity 100.0%; Pred. No. 6.3e-217;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

13 GGGCCACAGCAGCAGCTGCTGAGCCATGCGCTGAGGGGAAATCCACACCTTCACAGCC 72
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65 GGGCCACAGCAGCAGCTGCTGAGCCATGCGCTGAGGGGAAATCCACACCTTCACAGCC 124

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S-09-023-655-1390

## 65.5%; Score 418; DB 4; Length 490;

Best Local Similarity 100.0%; Pred. No. 1.4e-208;  
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QY 89 TCTGCTCCAGGGAATACAAAGACCCAACTCTCTCTAGTAGCAACGGGGCCACTT 148  
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QY 149 CTGAGAGATCTTCGGATGGCAAGTGGATGGGCAAGGAGCAGGAGCCAGCACAT 208  
Db 121 CTGAGAGATCTTCGGATGGCAAGTGGATGGGCAAGGAGCAGGAGCCAGCACAT 180  
QY 209 TCAGCTGAGCTCAGTGGGGAAGCTGGGGAGGTGTATATAAGAGTACCGAGACTG 268  
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QY 269 CCAGTACTTGGCCATGAGCAGCGAGGGCTTTTATAGGCTCAGACACCAATAGGA 328  
Db 241 CCAGTACTTGGCCATGAGCAGCGAGGGCTTTTATAGGCTCAGACACCAATAGGA 300  
QY 329 ATGTTTGTCTGGAAGGCTGAGGAGAACCAATCAACACTATATATCAAGAGCA 388  
Db 301 ATGTTTGTCTGGAAGGCTGAGGAGAACCAATCAACACTATATATCAAGAGCA 360  
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RESULT 3  
US-09-929-945-3  
; Sequence 3, Application US/09929945  
; Patent No. 6642026  
; GENERAL INFORMATION:  
; APPLICANT: Stegmarm, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svetlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Olexandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-929-945-3

Query Match 63.9%; Score 408; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 2.4e-203;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGCTGAGGGGAATACCACTTCAAGCCCTGACCGAAGTTTAACTGCTCCA 98  
Db 1 ATGCTGAGGGGAATACCACTTCAAGCCCTGACCGAAGTTTAACTGCTCCA 60  
QY 99 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 158  
Db 61 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 120  
QY 159 CTTCGGATGGCAAGTGGATGGGCAAGGAGCAGGAGCCAGCACATTCAGCTGCAG 218  
Db 121 CTTCGGATGGCAAGTGGATGGGCAAGGAGCAGGAGCCAGCACATTCAGCTGCAG 180  
QY 219 CTCAGTGGCAAGCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTACTTG 278  
Db 181 CTCAGTGGCAAGCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTACTTG 240  
QY 279 GCAATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGAGATGTTTGTTC 338  
Db 241 GCAATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGAGATGTTTGTTC 300

QY 339 CTGAAAGGCTGGAGGAGAACCTTACAAACCTATATATATCAAGAGCATGCGAGAG 398  
Db 301 CTGAAAGGCTGGAGGAGAACCTTACAAACCTATATATATCAAGAGCATGCGAGAG 360  
QY 399 AATTGTTGTGTTGGCTCAAGAAAGTGGAGCTGCAAAACGGGTCT 446  
Db 361 AATTGTTGTGTTGGCTCAAGAAAGTGGAGCTGCAAAACGGGTCT 408

RESULT 4  
US-08-793-900-1  
; Sequence 1, Application US/08793900  
; Patent No. 6143518  
; GENERAL INFORMATION:  
; APPLICANT: CAMERON, Beatrice  
; APPLICANT: CROUZET, Joel  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: PROTEINS, PLASMIDS AND MODIFIED CELLS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, Mailstop 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,900  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01178  
; FILING DATE: 14-SEP-1995  
; APPLICATION NUMBER: FR 94/11049  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky Esq., Martin F.  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: ST94069-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8501 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
US-08-793-900-1

Query Match 63.9%; Score 408; DB 3; Length 8501;  
Best Local Similarity 100.0%; Pred. No. 2.7e-203;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGCTGAGGGGAATACCACTTCAAGCCCTGACCGAAGTTTAACTGCTCCA 98  
Db 108 ATGCTGAGGGGAATACCACTTCAAGCCCTGACCGAAGTTTAACTGCTCCA 167  
QY 99 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 158  
Db 168 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 227  
QY 159 CTTCGGATGGCAAGTGGATGGGCAAGGAGCAGGAGCCAGCACATTCAGCTGCAG 218  
Db 228 CTTCGGATGGCAAGTGGATGGGCAAGGAGCAGGAGCCAGCACATTCAGCTGCAG 287  
QY 219 CTCAGTGGCAAGCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTACTTG 278  
Db 288 CTCAGTGGCAAGCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTACTTG 347  
QY 279 GCAATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGAGATGTTTGTTC 338  
Db 348 GCAATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGAGATGTTTGTTC 407

QY 339 CTGGAAGGCTGGAGGAGAACCACTTACACACCTATATATCCAGAGCATGCGAGAG 398  
DB 408 CTGGAAGGCTGGAGGAGAACCACTTACACACCTATATATCCAGAGCATGCGAGAG 467  
QY 399 AATTGGTTTGGCTTCAAGAGAAATGGAGCTGCAACCGCGTCT 446  
DB 468 AATTGGTTTGGCTTCAAGAGAAATGGAGCTGCAACCGCGTCT 515

RESULT 5  
5175147-1  
; Patent No. 5175147  
; APPLICANT: FOLKMAN, MOSES J.; KATO, KOICHI  
; TITLE OF INVENTION: ACID-RESISTANT FGF COMPOSITION AND METHOD  
; OF TREATING ULCERATING DISEASES OF THE GASTROINTESTINAL TRACT  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/382,263  
; FILING DATE: 20-JUL-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 234,966  
; FILING DATE: 19-AUG-1988  
; SEQ ID NO:1:  
; LENGTH: 454  
5175147-1

Query Match 29.2%; Score 186; DB 6; Length 454;  
Best Local Similarity 99.3%; Pred. No. 2.2e-87;  
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 159 CTTCGGATCGGACAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
DB 92 CTTCGGATCGGACAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 151  
QY 219 CTCAGTCCGGAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTGCCAGTACTTG 278  
DB 152 CTCAGTCCGGAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTGCCAGTACTTG 211  
QY 279 GCCATGACACCGCGGCTTTTATACGGCTCAGACACCAATAGGAATGTTGTC 338  
DB 212 GCATGACACCGCGGCTTTTATACGGCTCAGACACCAATAGGAATGTTGTC 271  
QY 339 CTGGAAGGCTGGAGGAGAACCACTTACACACCTATATATCCAGAGCATGCGAGAG 398  
DB 272 CTGGAAGGCTGGAGGAGAACCACTTACACACCTATATATCCAGAGCATGCGAGAG 331  
QY 399 AATTGGTTTGGCTTCAAGAGAAATGGAGCTGCAACCGCGTCT 446  
DB 332 AATTGGTTTGGCTTCAAGAGAAATGGAGCTGCAACCGCGTCT 379

RESULT 6  
5514566-3  
; Patent No. 5514566  
; APPLICANT: FIDDES, JOHN C.; ABRAHAM, JUDITH A.  
; TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT  
; FIBROBLASTS GROWTH FACTORS  
; NUMBER OF SEQUENCES: 21  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,022  
; FILING DATE: 05-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 809,163  
; FILING DATE: 16-DEC-1985  
; APPLICATION NUMBER: 775,521  
; FILING DATE: 12-SEP-1985  
; SEQ ID NO:3:  
; LENGTH: 197  
5514566-3

Query Match 27.0%; Score 172; DB 6; Length 197;  
Best Local Similarity 100.0%; Pred. No. 4.4e-80;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 36 GCCATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAGTGTAAATCTGCT 95  
DB 7 GCCATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAGTGTAAATCTGCT 66

QY 96 CACGGGAATTACAGAGAGCCCAACTCTCTCTACTGTAGCAACCGGGGCCACTTCTCTGAG 155  
DB 67 CACGGGAATTACAGAGAGCCCAACTCTCTCTACTGTAGCAACCGGGGCCACTTCTCTGAG 126  
QY 156 ATCTCTTCGGGATGCGACAGTGGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 207  
DB 127 ATCTCTTCGGGATGCGACAGTGGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 178

RESULT 7  
5437995-1  
; Patent No. 5437995  
; APPLICANT: ICHIMORI, YUZO; KONDO, KOICHI; IGARASHI, KOICHI;  
; SENDO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AGAINST AN ACIDIC  
; FGF PROTEIN AND HYBRIDOMA FOR ITS PRODUCTION  
; NUMBER OF SEQUENCES: 3  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/26,257  
; FILING DATE: 04-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 588,343  
; FILING DATE: 26-SEP-1990  
; SEQ ID NO:1:  
; LENGTH: 450  
5437995-1

Query Match 18.5%; Score 118; DB 6; Length 450;  
Best Local Similarity 100.0%; Pred. No. 7.4e-52;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 285 GACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGGAATGTTGTTCTGGAA 344  
DB 216 GACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGGAATGTTGTTCTGGAA 275  
QY 345 AGCTGGAGGAGAACCACTTATACACACCTTATATATCCAGAGCATGCGAGAGATT 402  
DB 276 AGCTGGAGGAGAACCACTTATACACACCTTATATATCCAGAGCATGCGAGAGATT 333

RESULT 8  
US-09-030-613-14  
; Sequence 14, Application US/09030613  
; Patent No. 6083706  
; GENERAL INFORMATION:  
; APPLICANT: Florikiewicz, Robert Z.  
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,613  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6083706tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.418C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 454 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-030-613-14

Query Match 12.1%; Score 77; DB 3; Length 454;  
Best Local Similarity 100.0%; Pred. No. 1.9e-30;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 282 ATGGACACCGGCGCTTTTATACGGCTCAGACACCAAAATGAGGAATGTTGTTCTG 341  
Db 246 ATGGACACCGGCGCTTTTATACGGCTCAGACACCAAAATGAGGAATGTTGTTCTG 305  
QY 342 GAAAGCGCTGGAGGAGAA 358  
Db 306 GAAAGCGCTGGAGGAGAA 322

RESULT 9  
US-09-451-905-14  
; Sequence 14, Application US/09451905  
; Patent No. 6306613  
; GENERAL INFORMATION:  
; APPLICANT: Robert Z. Florkiewicz  
; APPLICANT: Andrew Baird  
; APPLICANT: Dale E. Warnock  
; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
; FILE REFERENCE: 200124.402C4  
; CURRENT APPLICATION NUMBER: US/09/451.905  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 454  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-451-905-14

Query Match 12.1%; Score 77; DB 4; Length 454;  
Best Local Similarity 100.0%; Pred. No. 1.9e-30;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 282 ATGGACACCGGCGCTTTTATACGGCTCAGACACCAAAATGAGGAATGTTGTTCTG 341  
Db 246 ATGGACACCGGCGCTTTTATACGGCTCAGACACCAAAATGAGGAATGTTGTTCTG 305  
QY 342 GAAAGCGCTGGAGGAGAA 358  
Db 306 GAAAGCGCTGGAGGAGAA 322

RESULT 10  
US-09-929-945-1  
; Sequence 1, Application US/09929945  
; Patent No. 6642026  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: CYGEN.008A  
; CURRENT APPLICATION NUMBER: US/09/929.945  
; NUMBER OF SEQ ID NOS: 8  
; CURRENT FILING DATE: 2001-08-15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized sequence for human acidic  
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
; OTHER INFORMATION: preferred codons for E. coli  
; NAME/KEY: CDS  
; LOCATION: (122)...(590)  
US-09-929-945-1

Query Match 4.1%; Score 26; DB 4; Length 630;  
Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAATCACCACCTT 64  
Db 122 ATGGCTGAAGGGGAATCACCACCTT 147

RESULT 11  
5514566-1  
; Patent No. 5514566  
; APPLICANT: FIDES, JOHN C.; ABRAHAM, JUDITH A.  
; TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT  
; FIBROBLAST GROWTH FACTORS  
; NUMBER OF SEQUENCES: 21  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,022  
; FILING DATE: 05-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 809,163  
; FILING DATE: 16-DEC-1985  
; APPLICATION NUMBER: 775,521  
; FILING DATE: 12-SEP-1985  
; SEQ ID NO: 1  
; LENGTH: 270  
5514566-1

Query Match 3.8%; Score 24; DB 6; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.0092;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 26 CAGCTGCTGAGCCATGCTCAAGG 49  
Db 9 CAGCTGCTGAGCCATGCTCAAGG 32

RESULT 12  
US-08-023-757-8  
; Sequence 8, Application US/08023757  
; Patent No. 5302702  
; GENERAL INFORMATION:  
; APPLICANT: Seddon Dr., Andrew P.  
; APPLICANT: Bohlen Dr., Peter  
; APPLICANT: Gluzman Dr., Yakov  
; TITLE OF INVENTION: Chimeric Fibroblast Growth Factors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: 1937 West Main Street, P. O. Box 60  
; CITY: Stamford,  
; STATE: CT  
; COUNTRY: USA  
; ZIP: 06904-0060  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/023,757  
; FILING DATE: 26-FEB-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/615,202  
; FILING DATE: 23-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tsevdos Dr., Estelle J.  
; REGISTRATION NUMBER: 31,145  
; REFERENCE/DOCKET NUMBER: 31,219-00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203-321-2756  
; TELEFAX: 203-321-2971  
; TELEX: 710-474-4059  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
US-08-023-757-8

Query Match 3.6%; Score 23; DB 1; Length 44;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAATCACCAC 61  
|||||  
Db 9 ATGGCTGAAGGGGAATCACCAC 31

#### RESULT 13

US-08-177-502-8  
Sequence 8, Application US/08177502  
Patent No. 5371206

#### GENERAL INFORMATION:

APPLICANT: Seddon Dr., Andrew P.  
APPLICANT: Bohlen, Peter  
TITLE OF INVENTION: Chimeric Fibroblast Growth Factors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: 1937 West Main Street, P. O. Box 60  
CITY: Stamford,  
STATE: CT  
COUNTRY: USA  
ZIP: 06904-0060

#### COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/177,502  
FILING DATE: 05-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/023,757  
FILING DATE: 26-FEB-1993  
APPLICATION NUMBER: US/07/615,202  
FILING DATE: 23-NOV-1990

#### ATTORNEY/AGENT INFORMATION:

NAME: Tsevdos Dr., Estelle J.  
REGISTRATION NUMBER: 31,145  
REFERENCE/DOCKET NUMBER: 31,219-00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-321-2756  
TELEFAX: 203-321-2971  
TELEX: 710-474-4059  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
US-08-177-502-8

Query Match 3.6%; Score 23; DB 1; Length 44;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAATCACCAC 61  
|||||  
Db 9 ATGGCTGAAGGGGAATCACCAC 31

#### RESULT 14

US-08-054-650A-2  
Sequence 2, Application US/08054650A

Patent No. 5387673  
GENERAL INFORMATION:  
APPLICANT: Seddon, Andrew P.  
APPLICANT: Bohlen, Peter  
TITLE OF INVENTION: Active Fragments of Fibroblast Growth  
TITLE OF INVENTION: Factor  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anne M. Rosenblum  
STREET: 163 Delaware Avenue, Suite 212  
CITY: Delmar  
STATE: New York  
COUNTRY: USA  
ZIP: 12054

#### COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/054,650A  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Tsevdos, Estelle J.  
REGISTRATION NUMBER: 31145  
REFERENCE/DOCKET NUMBER: 31309-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (518)475-0611  
TELEFAX: (518)475-0619  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-054-650A-2

Query Match 3.6%; Score 23; DB 1; Length 44;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAATCACCAC 61  
|||||  
Db 9 ATGGCTGAAGGGGAATCACCAC 31

#### RESULT 15

US-08-383-621-11  
Sequence 11, Application US/08383621  
Patent No. 5951972

#### GENERAL INFORMATION:

APPLICANT: Daley, Michael J.  
APPLICANT: Buckwalter, Brian L.  
APPLICANT: Cady, Susan M.  
APPLICANT: Shieh, Hong-Ming  
APPLICANT: Bohlen, Peter  
APPLICANT: Seddon, Andrew P.  
TITLE OF INVENTION: Stabilization Of Somatotropins And Other  
TITLE OF INVENTION: Proteins By Modification Of Cysteine Residues  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Estelle J. Tsevdos  
STREET: 1937 West Main Street, P.O. Box 60  
CITY: Stamford  
STATE: Connecticut  
COUNTRY: U.S.A.  
ZIP: 06904-0060

#### COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/383,621  
FILING DATE: 06-FEB-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/766,142  
 FILING DATE: 25-SEP-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Tsevdos, Estelle J.  
 REGISTRATION NUMBER: 31,145  
 REFERENCE/DOCKET NUMBER: 31,278-01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 203-321-2756  
 TELEFAX: 203-321-2971  
 TELEX: 203-710-474-4059  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 44 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-383-621-11

Query Match 3.6%; Score 23; DB 2; Length 44;  
 Best local similarity 100.0%; Pred.No. 0.028;  
 Matches 23; Conservative 0; Mismatches 0; Gaps 0;

QY 39 ATGCTGAAGGGGAATCCAC 61  
 |||||  
 Db 9 ATGCTGAAGGGGAATCCAC 31

Search completed: August 24, 2004, 23:07:01  
 Job time : 87 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 21:00:28 ; Search time 482 Seconds  
 (without alignments)  
 6501.952 Million cell updates/sec

Title: US-10-022-554A-3

Perfect score: 638  
 Sequence: 1 gaattcggaacgcgcaca.....ctgaatttgaagcaactt 638

Scoring table: OLIGO NUC  
 Gapop 60.0 , Gapext 60.0

Searched: 3228839 seqs, 245606551 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6457678

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB.seq:\*

18: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq:\*

19: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	434	68.0	638	10	US-09-902-460-3	Sequence 3, Appli
2	434	68.0	4087	14	US-10-044-090-225	Sequence 225, App
3	418	65.5	490	15	US-10-388-410-8	Sequence 8, Appli
4	418	65.5	490	17	US-10-641-643-1390	Sequence 1390, Ap
5	408	63.9	468	9	US-09-929-918-3	Sequence 3, Appli
6	408	63.9	468	9	US-09-929-945-3	Sequence 3, Appli
7	408	63.9	468	15	US-10-280-864-3	Sequence 3, Appli
8	408	63.9	468	17	US-10-649-480-3	Sequence 3, Appli
C 9	195	30.6	580	9	US-09-864-761-13391	Sequence 13391, A
C 10	187	29.3	187	9	US-09-864-761-29943	Sequence 29943, A
11	147	23.0	478	16	US-10-116-275-235	Sequence 235, App
12	135	21.2	3658	12	US-09-968-007A-133	Sequence 133, App
13	135	21.2	3658	12	US-09-968-007A-440	Sequence 440, App
14	26	4.1	65	10	US-09-908-975-28515	Sequence 28515, A
15	26	4.1	630	9	US-09-929-918-1	Sequence 1, Appli
16	26	4.1	630	9	US-09-929-945-1	Sequence 1, Appli
17	26	4.1	630	15	US-10-280-864-1	Sequence 1, Appli
18	26	4.1	630	17	US-10-649-480-1	Sequence 1, Appli
19	26	4.1	990	9	US-09-929-918-10	Sequence 10, Appli
20	22	3.4	29	10	US-09-847-936B-13	Sequence 13, Appli
C 21	21	3.3	28	10	US-09-847-936B-12	Sequence 12, Appli
22	21	3.3	630	9	US-09-929-918-4	Sequence 4, Appli
23	21	3.3	630	9	US-09-929-918-6	Sequence 6, Appli
24	21	3.3	630	9	US-09-929-945-4	Sequence 4, Appli
25	21	3.3	630	9	US-09-929-945-6	Sequence 6, Appli
26	21	3.3	630	15	US-10-280-864-4	Sequence 4, Appli
27	21	3.3	630	15	US-10-280-864-6	Sequence 6, Appli
28	21	3.3	630	17	US-10-649-480-4	Sequence 4, Appli
29	21	3.3	630	17	US-10-649-480-6	Sequence 6, Appli
30	20	3.1	20	10	US-09-981-803-19	Sequence 19, Appli
31	20	3.1	20	15	US-10-104-025-1	Sequence 1, Appli
C 32	20	3.1	637	13	US-10-027-632-188645	Sequence 188645,
C 33	20	3.1	637	13	US-10-027-632-188646	Sequence 188646,
C 34	20	3.1	637	16	US-10-027-632-188645	Sequence 188645,
C 35	20	3.1	637	16	US-10-027-632-188646	Sequence 188646,
36	19	3.0	581	9	US-09-864-761-9138	Sequence 9138, Ap
C 37	19	3.0	1231	17	US-10-437-963-22726	Sequence 22726, A
C 38	19	3.0	2121	17	US-10-437-963-64740	Sequence 64740, A
39	19	3.0	2715	9	US-09-764-870-65	Sequence 65, Appli
40	19	3.0	2715	15	US-10-125-540-65	Sequence 84, Appli
C 41	19	3.0	4270	15	US-10-000-256A-84	Sequence 473, App
42	19	3.0	4715	13	US-10-296-115-473	Sequence 182, App
43	19	3.0	5111	13	US-10-342-887-182	Sequence 182, App
44	19	3.0	5111	13	US-10-172-118-182	Sequence 1, Appli
C 45	19	3.0	2256646	17	US-10-470-565-1	Sequence 1, Appli

# ALIGNMENTS

RESULT 1  
 US-09-902-460-3  
 ; Sequence 3, Application US/09902460  
 ; Publication No. US20030040042A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FIDDES, J.C.  
 ; ABRAM, J.D.  
 ; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH  
 ; FACTOR ANALOG  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FORESTER  
 ; STREET: 755 PAGE MILL ROAD  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018





Db 1 CTGCTGAGCCATCGCTGAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAA 60  
 QY 89 TCTGCTCCAGGGAAATACAGAGCCCAAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 148  
 Db 61 TCTGCTCCAGGGAAATACAGAGCCCAAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 QY 149 CTGAGGATCTCTTCGGATGGCAGTGGATGGGACAGGAGGACAGGAGGACAGGAGGACAT 208  
 Db 121 CTGAGGATCTCTTCGGATGGCAGTGGATGGGACAGGAGGACAGGAGGACAGGAGGACAT 180  
 QY 209 TCAGCTGACCTAGTGGGAAAGCGTGGGGAGAGGTGTATATAAGAGTACCGAGACTGG 268  
 Db 181 TCAGCTGACCTAGTGGGAAAGCGTGGGGAGAGGTGTATATAAGAGTACCGAGACTGG 240  
 QY 269 CCAGTACTTGGCCATGACACCGAGCGGCTTTTATACGGCTCACAGACACCAATGAGGA 328  
 Db 241 CCAGTACTTGGCCATGACACCGAGCGGCTTTTATACGGCTCACAGACACCAATGAGGA 300  
 QY 329 ATGTTTCTCTGAAAGGCTGGAGGAGAACCAATTAACAACCTATATATCCAAAGCA 388  
 Db 301 ATGTTTCTCTGAAAGGCTGGAGGAGAACCAATTAACAACCTATATATCCAAAGCA 360  
 QY 389 TGCAGAGAAGATGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAACGGGTCT 446  
 Db 361 TGCAGAGAAGATGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAACGGGTCT 418

#### RESULT 4

US-10-641-643-1390  
 ; Sequence 1390, Application US/10641643  
 ; Publication No. US20040077003A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; Jeffrey J. Seilhamer  
 ; Susan G. Stuart  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
 ; GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/641,643  
 ; FILING DATE: 14-Aug-2003  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: <Unknown>  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1390:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 490 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: g396163  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1390 :  
 US-10-641-643-1390

Query Match 65.5%; Score 418; DB 17; Length 490;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-207;

Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 29 CTGCTGAGCCATCGCTGAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAA 88  
 Db 1 CTGCTGAGCCATCGCTGAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAA 60  
 QY 89 TCTGCTCCAGGGAAATACAGAGCCCAAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 148  
 Db 61 TCTGCTCCAGGGAAATACAGAGCCCAAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 QY 149 CTGAGGATCTCTTCGGATGGCAGTGGATGGGACAGGAGGACAGGAGGACAGGAGGACAT 208  
 Db 121 CTGAGGATCTCTTCGGATGGCAGTGGATGGGACAGGAGGACAGGAGGACAGGAGGACAT 180  
 QY 209 TCAGCTGACCTAGTGGGAAAGCGTGGGGAGAGGTGTATATAAGAGTACCGAGACTGG 268  
 Db 181 TCAGCTGACCTAGTGGGAAAGCGTGGGGAGAGGTGTATATAAGAGTACCGAGACTGG 240  
 QY 269 CCAGTACTTGGCCATGACACCGAGCGGCTTTTATACGGCTCACAGACACCAATGAGGA 328  
 Db 241 CCAGTACTTGGCCATGACACCGAGCGGCTTTTATACGGCTCACAGACACCAATGAGGA 300  
 QY 329 ATGTTTCTCTGAAAGGCTGGAGGAGAACCAATTAACAACCTATATATCCAAAGCA 388  
 Db 301 ATGTTTCTCTGAAAGGCTGGAGGAGAACCAATTAACAACCTATATATCCAAAGCA 360  
 QY 389 TGCAGAGAAGATGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAACGGGTCT 446  
 Db 361 TGCAGAGAAGATGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAACGGGTCT 418

#### RESULT 5

US-09-929-918-3  
 ; Sequence 3, Application US/09929918  
 ; Patent No. US20020090678A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kordyum, Vitaliy A.  
 ; APPLICANT: Chernykh, Svilana I.  
 ; APPLICANT: Slavchenko, Iryna Yu.  
 ; APPLICANT: Vozianov, Olexandr  
 ; TITLE OF INVENTION: PHASE-DEPENDENT SUPER PRODUCTION OF  
 ; FILE REFERENCE: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES  
 ; CURRENT APPLICATION NUMBER: US/09/929,918  
 ; CURRENT FILING DATE: 2001-08-15  
 ; PRIOR FILING DATE: 09/318,288  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 468  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-929-918-3

Query Match 63.9%; Score 408; DB 9; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-201;  
 Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 39 ATGCGTGAAGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAACTGCTCCA 98  
 Db 1 ATGCGTGAAGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAACTGCTCCA 60  
 QY 99 GGGAAATTAAGAAGCCCAAACT 158  
 Db 61 GGGAAATTAAGAAGCCCAAACT 120  
 QY 159 CTTCGGATGGCAGTGGATGGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
 Db 121 CTTCGGATGGCAGTGGATGGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 QY 219 CTCAGTGGCGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCAGTCTTG 278  
 Db 181 CTCAGTGGCGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCAGTCTTG 240  
 QY 279 GCGATGACACCGAGCGGCTTTTATACGGCTCACAGACACCAATGAGGAATGTTGTTTC 338  
 Db 241 GCGATGACACCGAGCGGCTTTTATACGGCTCACAGACACCAATGAGGAATGTTGTTTC 300

QY 339 CTGGAAGGCTGGAGGAGAACCAATTACACACCTATATATCCAGAGCATCGAGAG 398  
Db 301 CTGGAAGGCTGGAGGAGAACCAATTACACACCTATATATCCAGAGCATCGAGAG 360  
QY 399 AATGCTGTTGTTGGCTCAAGAGAAATGGAGCTGCAAGCGGCTCT 446  
Db 361 AATGCTGTTGTTGGCTCAAGAGAAATGGAGCTGCAAGCGGCTCT 408

#### RESULT 6

US-09-929-945-3  
; Sequence 3, Application US/0929945  
; Patent No. US2002015532A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-929-945-3

Query Match 63.9%; Score 408; DB 9; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.3e-201;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
Db 1 ATGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 60  
QY 99 GCGAATTACAGAGCCCAACTCTCTACTGTAGCAAGCGGGCCACTTCTCGAGATC 158  
Db 61 GCGAATTACAGAGCCCAACTCTCTACTGTAGCAAGCGGGCCACTTCTCGAGATC 120  
QY 159 CTTCGGATGGCAAGTGGATGGCAAGGGACAGGAGCGACACCATTCAGCTGCAG 218  
Db 121 CTTCGGATGGCAAGTGGATGGCAAGGGACAGGAGCGACACCATTCAGCTGCAG 180  
QY 219 CTGAGTGGCAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTGCGAGTCTTG 278  
Db 181 CTGAGTGGCAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTGCGAGTCTTG 240  
QY 279 GCGATGACACCGAGCGGCTTTTATACGGCTCACAGACCAAAATGAGGAATGTTTTC 338  
Db 241 GCGATGACACCGAGCGGCTTTTATACGGCTCACAGACCAAAATGAGGAATGTTTTC 300  
QY 339 CTGGAAGGCTGGAGGAGAACCAATTACACACCTATATATCCAGAGCATCGAGAG 398  
Db 301 CTGGAAGGCTGGAGGAGAACCAATTACACACCTATATATCCAGAGCATCGAGAG 360  
QY 399 AATGCTGTTGTTGGCTCAAGAGAAATGGAGCTGCAAGCGGCTCT 446  
Db 361 AATGCTGTTGTTGGCTCAAGAGAAATGGAGCTGCAAGCGGCTCT 408

#### RESULT 7

US-10-280-864-3  
; Sequence 3, Application US/10280864  
; Publication No. US2003005492A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/10/280,864

; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: US/09/929,945  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-280-864-3

Query Match 63.9%; Score 408; DB 15; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.3e-201;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
Db 1 ATGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 60  
QY 99 GCGAATTACAGAGCCCAACTCTCTACTGTAGCAAGCGGGCCACTTCTCGAGATC 158  
Db 61 GCGAATTACAGAGCCCAACTCTCTACTGTAGCAAGCGGGCCACTTCTCGAGATC 120  
QY 159 CTTCGGATGGCAAGTGGATGGCAAGGGACAGGAGCGACACCATTCAGCTGCAG 218  
Db 121 CTTCGGATGGCAAGTGGATGGCAAGGGACAGGAGCGACACCATTCAGCTGCAG 180  
QY 219 CTGAGTGGCAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTGCGAGTCTTG 278  
Db 181 CTGAGTGGCAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTGCGAGTCTTG 240  
QY 279 GCGATGACACCGAGCGGCTTTTATACGGCTCACAGACCAAAATGAGGAATGTTTTC 338  
Db 241 GCGATGACACCGAGCGGCTTTTATACGGCTCACAGACCAAAATGAGGAATGTTTTC 300  
QY 339 CTGGAAGGCTGGAGGAGAACCAATTACACACCTATATATCCAGAGCATCGAGAG 398  
Db 301 CTGGAAGGCTGGAGGAGAACCAATTACACACCTATATATCCAGAGCATCGAGAG 360  
QY 399 AATGCTGTTGTTGGCTCAAGAGAAATGGAGCTGCAAGCGGCTCT 446  
Db 361 AATGCTGTTGTTGGCTCAAGAGAAATGGAGCTGCAAGCGGCTCT 408

#### RESULT 8

US-10-649-480-3  
; Sequence 3, Application US/10649480  
; Publication No. US20040115769A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/10/649,480  
; CURRENT FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: 10/649,480  
; PRIOR FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-649-480-3

Query Match 63.9%; Score 408; DB 17; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.3e-201;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
Db 1 ATGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 60  
QY 99 GCGAATTACAGAGCCCAACTCTCTACTGTAGCAAGCGGGCCACTTCTCGAGATC 158

Db 61 GGGAAATTACAGAGCCCAACTCTCTACTACTAGCAGCGGGGCGCACTCTCTGAGATC 120  
QY 159 CTTCCCGATGGCACTGATGGGACAGAGGAGGACGACGACCAATCAGCTGGAG 218  
Db 121 CTTCCCGATGGCACTGATGGGACAGAGGAGGACGACGACCAATCAGCTGGAG 180  
QY 219 CTCAGTGGCGAAAGCGTGGGGAGGCTGTATATAAGAGTACCGGACCTGACCTACTTG 278  
Db 181 CTCAGTGGCGAAAGCGTGGGGAGGCTGTATATAAGAGTACCGGACCTGACCTACTTG 240  
QY 279 CCATGAGCACCGACCGGCTTTTATACGGCTTCACAGACCAATGAGGATGTTTGTTC 338  
Db 241 CCATGAGCACCGACCGGCTTTTATACGGCTTCACAGACCAATGAGGATGTTTGTTC 300  
QY 339 CTGGAAGGCTGGAGGAGAACATTACAAACCTTATATATCAAGAGTACGACGAGAG 398  
Db 301 CTGGAAGGCTGGAGGAGAACATTACAAACCTTATATATCAAGAGTACGACGAGAG 360  
QY 399 AATTGGTTTGTGGCTTCAAGAGATGGGAGCTGCAAAACGGGTCT 446  
Db 361 AATTGGTTTGTGGCTTCAAGAGATGGGAGCTGCAAAACGGGTCT 408

RESULT 9  
US-09-864-761-13391/c  
; Sequence 13391, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aemica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; LENGTH: 580  
; TYPE: DNA

; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC010489.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1  
US-09-864-761-13391

Query Match 30.6%; Score 195; DB 9; Length 580;  
Best Local Similarity 100.0%; Pred. No. 8.le-91;  
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGCCACAGCAGCAGCAGCTGCTGAGCCATGCTGAGAGGGGAATCCACCTTCACAGCC 72  
Db 272 GCGCCACAGCAGCAGCAGCTGCTGAGCCATGCTGAGAGGGGAATCCACCTTCACAGCC 213  
QY 73 TGACCCGAGAGTTTAACTCTCCAGGGAATTCAGAGAGCCCAAACTCTCTACTGTA 132  
Db 212 TGACCCGAGAGTTTAACTCTCCAGGGAATTCAGAGAGCCCAAACTCTCTACTGTA 153  
QY 133 GCAACGGGGGCGACCTCTCTGAGATTCCTTCGGATGTCACAGTGGGACAGGACA 192  
Db 152 GCAACGGGGGCGACCTCTCTGAGATTCCTTCGGATGTCACAGTGGGACAGGACA 93  
QY 193 GGAGCGACAGCAGCA 207  
Db 92 GGAGCGACAGCAGCA 78

RESULT 10  
US-09-864-761-29943/c  
; Sequence 29943, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aemica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR FILING DATE: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
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; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117

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; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29943
; LENGTH: 187
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010489.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EST HUMAN HIT: A1590078.1, EVALUE 1.00e-101
; OTHER INFORMATION: SWISSPROT HIT: P05230, EVALUE 6.00e-29
; OTHER INFORMATION: NT HIT: G111416219, EVALUE 1.00e-101
US-09-864-761-29943

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Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ASCAGAGCTGCTGAGCATGCTGCAAGGGGAATTCACCACTTCACAGCCCTGACCGAG 80
Db |||||
QY 187 ACAGCAGCTGCTGAGCATGCTGCAAGGGGAATTCACCACTTCACAGCCCTGACCGAG 128
Db |||||
QY 81 AAGTTTAAATCTGCTCCAGGGAATTCACGAAGCCCAAACTCTCTACTGTAGCAAGGG 140
Db |||||
QY 127 AAGTTTAAATCTGCTCCAGGGAATTCACGAAGCCCAAACTCTCTACTGTAGCAAGGG 168
Db |||||
QY 141 GGCACACTTCTGAGATCTCTCCGATGGCAGTGGATGGGACAGGACAGGAGCGAC 200
Db |||||
QY 67 GGCACACTTCTGAGATCTCTCCGATGGCAGTGGATGGGACAGGAGCGAC 8
Db |||||
QY 201 CAGCAC 207
Db |||||
QY 7 CAGCAC 1

RESULT 11
US-10-116-275-235
; Sequence 235, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods
and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116.275
; CURRENT FILING DATE: 2002-10-04
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 349
; SEQ ID NO 235
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-275-235

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Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGCCACAGCAGCAGCTCTGAGCATGCTGAGGGGAATTCACGAAGCCCAAACTCTCTACTGTA 132
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QY 332 GCGCCACAGCAGCAGCTCTGAGCATGCTGAGGGGAATTCACGAAGCCCAAACTCTCTACTGTA 391
Db |||||
QY 73 TGACCGAGAAGTTTAAATCTGCTCCAGGGAATTCACGAAGCCCAAACTCTCTACTGTA 132
Db |||||
QY 392 TGACCGAGAAGTTTAAATCTGCTCCAGGGAATTCACGAAGCCCAAACTCTCTACTGTA 451
Db |||||
QY 133 GCACAGGGGGCCCTCCGAGGATCC 159
Db |||||
QY 452 GCACAGGGGGCCCTCCGAGGATCC 478
Db |||||

RESULT 12
US-09-968-007A-133
; Sequence 133, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
Signature
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968.007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 440
; LENGTH: 3658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-440

Query Match      21.2%; Score 135; DB 12; Length 3658;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 CAGACCAAAATGAGGAATTTTGTCTCGAAAGGCTTGGAGGAGAACCACTTACACACC 371
Db |||||
QY 304 CAGACCAAAATGAGGAATTTTGTCTCGAAAGGCTTGGAGGAGAACCACTTACACACC 363
Db |||||
QY 372 TATATATCAAGAAGCATGCAAGAGAGATTTGTTTGTCTCGAAAGGCTTGGAGGAGAACCACTTACACACC 431
Db |||||
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Db |||||
QY 432 TGCAACGCGGCTCT 446
Db |||||
QY 424 TGCAACGCGGCTCT 438
Db |||||

RESULT 13
US-09-968-007A-440
; Sequence 440, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
Signature
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968.007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 440
; LENGTH: 3658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-440

Query Match      21.2%; Score 135; DB 12; Length 3658;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; OTHER INFORMATION: codons which are used in highly expressed proteins from E.
coli.
; NAME/KEY: CDS
; LOCATION: (122)...(590)
US-09-929-918-1

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      122  ATGGCTGAAGGGGAATCACCACCTT 147

Search completed: August 24, 2004, 23:15:18
Job time : 485 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

LOW nucleic - nucleic search, using sw model

Run on:      August 24, 2004, 20:50:43 ; Search time 2845 Seconds
              (without alignments)
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6696.686 Million cell updates/sec

Title: US-10-022-554A-3
Perfect score: 638
Sequence: 1 gaattcggaacgcgcacac.....cctgaatttgaaacactt 638

Scoring table: OLIGO NTC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Post-processing: Listing first 45 summaries

Database : EST \*

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7: em_estro:*
8: em_hlc:*
9: gb_est1:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

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Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
    Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
    found through the I.M.A.G.E. Consortium/ILMIL at:  
    www-bio11.gwi.gov/bbrp/image/image.html  
Insert length: 736     Std Error: 0.00  
Gap primer: -40UP from Gibco  
High quality sequence stop: 455.

## FEATURES

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7	317	49.7	522	14	CD701495	EDT18019
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30	72	11.3	588	12	BQ060606	UI-H-E11-
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36	59	9.2	313	29	CG605210	OST37278
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39	59	9.2	346	13	BX141229	BY317992
40	59	9.2	358	13	BX102462	BY141229
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DEFINITION	similar to gb:U131361 HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN);, mRNA sequence.				
ACCESSION	AI590078				
VERSION	AI590078.1	GI:4599126			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/STGAP), Tumor Gene Index				
JOURNAL	Unpublished (1998)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 821)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-f@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1764 row: k column: 23  
High quality sequence stop: 777.

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primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NIHRI, National Institutes of Health). Note: this is  
a NIH MGC Library."

ORIGIN  
Query Match 68.0%; Score 434; DB 12; Length 821;  
Best Local Similarity 100.0%; Pred. No. 2.4e-211;  
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QY 133 GCAACGGGGGCCCTCTCTGAGGATCTTCGCGATGGCAGTGGATGGGACAGGGACA 192  
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QY 193 GGAGCCACAGCAGCAGTGGCAGTCTGAGGATCTTCGCGATGGCAGTGGATGGGACAGGGACA 353  
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QY 373 ATATATCCAGAGCATGCGAGAGATTTGGTTTGTGGCTTCAAGAGATGGGAGCT 432  
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RESULT 3  
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LOCUS  
1014 bp mRNA linear EST 05-MAR-2002

AGENCY: NIH-MGC\_124 Homo sapiens cDNA clone IMAGE:5734445  
5', mRNA sequence.  
BM809005  
VERSION  
BM809005.1 GI:19125828  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
1 (bases 1 to 1014)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-f@mail.nih.gov  
Tissue Procurement: Invitrogen  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1739 row: m column: 06  
High quality sequence stop: 637.

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cloned (EcoRV site is destroyed upon cloning). Average  
insert size 1.4 kb, insert size range 0.9-4 kb. Library is  
normalized and enriched for full-length clones and was  
constructed by C. Gruber (Invitrogen). Research Genetics  
tracking code 012."

ORIGIN  
Query Match 68.0%; Score 434; DB 12; Length 1014;  
Best Local Similarity 100.0%; Pred. No. 2.5e-211;  
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QY 193 GGAGCCACAGCAGCAGTGGCAGTCTGAGGATCTTCGCGATGGCAGTGGATGGGACAGGGACA 352  
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QY 253 AGATGACAGCAGTGGCAGTCTGAGGATCTTCGCGATGGCAGTGGATGGGACAGGGACA 312  
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QY 373 ATATATCCAGAGCATGCGAGAGATTTGGTTTGTGGCTTCAAGAGATGGGAGCT 432  
DB 517 ATATATCCAGAGCATGCGAGAGATTTGGTTTGTGGCTTCAAGAGATGGGAGCT 476  
QY 433 GCAACGGGGTCTCT 446  
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BM809005  
LOCUS  
1014 bp mRNA linear EST 05-MAR-2002



RESULT 4  
 BQ067949  
 LOCUS  
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 ACCESSION BQ067949  
 VERSION BQ067949.1 GI:19896995  
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 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 NIH-MGC http://mgi.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Cloning Strategy: Agencourt Bioscience Corporation  
 Cloning Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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 and male age 26 weeks. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.7 kb, insert size range  
 0.7-3.5 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 017. Note:  
 this is a NIH\_MGC Library."

# ORIGIN

Query Match 68.0%; Score 434; DB 13; Length 1057;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-211;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 GCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTTCACAGCCC 72  
 Db 115 GCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTTCACAGCCC 174  
 QY 73 TGACCGAGAAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 132  
 Db 175 TGACCGAGAAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 234  
 QY 133 GCACGGGGGGCCACTTCTCGAGGATCTTCGGATGGCAGTCAGTGGGACCAAGGACA 192  
 Db 235 GCACGGGGGGCCACTTCTCGAGGATCTTCGGATGGCAGTCAGTGGGACCAAGGACA 294  
 QY 193 GGAGCAGCAGCAGCATTTACAGCTCAGTCAGTGGGAAAGCGTGGGGAGGTGTATATTA 252  
 Db 295 GGAGCAGCAGCAGCATTTACAGCTCAGTCAGTGGGAAAGCGTGGGGAGGTGTATATTA 354  
 QY 253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTAC 312  
 Db 355 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTAC 414  
 QY 313 AGACACCAATTCAGGAATGTTTGTCTCGAAAGCTTGGAGAGACCAATTACACACT 372  
 Db 415 AGACACCAATTCAGGAATGTTTGTCTCGAAAGCTTGGAGAGACCAATTACACACT 474  
 QY 373 ATATATCCAAAGACATGCAGAGAAGATTGGTTTGTGGCTTCAAGAAGATGGAGCT 432  
 Db 475 ATATATCCAAAGACATGCAGAGAAGATTGGTTTGTGGCTTCAAGAAGATGGAGCT 534

QY 433 GCACCAAGCGGTCTT 446  
 Db 535 GCACCAAGCGGTCTT 548  
 RESULT 5  
 BQ444567  
 LOCUS  
 DEFINITION BQ444567 1173 bp mRNA linear EST 15-MAY-2003  
 CSODN003YP16 5-PRIME, mRNA sequence.  
 ACCESSION BQ444567  
 VERSION BQ444567.1 GI:30780253  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1. (bases 1 to 1173)  
 Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 JOURNAL  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 3201.r for  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODN003DH08QPlaccluster=3201.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODN003DH08QPl.  
 Location/Qualifiers  
 1. .1173  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSODN003YP16"  
 /tissue\_type="ADULT BRAIN"  
 /dev\_stage="adult"  
 /clone\_lib="Homo sapiens ADULT BRAIN"  
 /note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

# ORIGIN

Query Match 68.0%; Score 434; DB 13; Length 1173;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-211;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 GCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTTCACAGCCC 72  
 Db 142 GCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTTCACAGCCC 201  
 QY 73 TGACCGAGAAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 132  
 Db 202 TGACCGAGAAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 261  
 QY 133 GCACGGGGGGCCACTTCTCGAGGATCTTCGGATGGCAGTCAGTGGGACCAAGGACA 192  
 Db 262 GCACGGGGGGCCACTTCTCGAGGATCTTCGGATGGCAGTCAGTGGGACCAAGGACA 321  
 QY 193 GGAGCAGCAGCAGCATTTACAGCTCAGTCAGTGGGAAAGCGTGGGGAGGTGTATATTA 252  
 Db 322 GGAGCAGCAGCAGCATTTACAGCTCAGTCAGTGGGAAAGCGTGGGGAGGTGTATATTA 381  
 QY 253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTAC 312  
 Db 382 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTAC 441  
 QY 313 AGACACCAATTCAGGAATGTTTGTCTCGAAAGCTTGGAGAGACCAATTACACACT 372  
 Db 442 AGACACCAATTCAGGAATGTTTGTCTCGAAAGCTTGGAGAGACCAATTACACACT 501  
 QY 373 ATATATCCAAAGACATGCAGAGAAGATTGGTTTGTGGCTTCAAGAAGATGGAGCT 432

```

Db      502 ATATATCCAAAGACATGCAGAGAAATGTGTTTGCTTCAAGAGATGGAGCT 561
QY      433 GCAAGCGGCTCT 446
Db      562 GCAACGCGGCTCT 575

RESULT 6
B1869731
LOCUS   601393620F1.NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5403677 5',
DEFINITION
ACCESSION B1869731
VERSION   B1869731.1 GI:16043404
KEYWORDS  mRNA sequence.
SOURCE    EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 832)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Life Technologies, Inc.
          CDNA Sequencing by: The I.M.A.G.E. Consortium (ILML)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/ILML at:
          http://image.llnl.gov
          Plate: L1AM12029 row: 9 column: 06
          High quality sequence stop: 829.

FEATURES             Location/Qualifiers
     source            1..832
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5403677"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_90"
                     /notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.7 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."

ORIGIN
Query Match      50.3%; Score 321; DB 12; Length 832;
Best Local Similarity 100.0%; Pred. No. 2.6e-153;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

13  GCGCCACAACGACGAGCTGCTGAGCGCATGCTGAGGGGAAATCACCACTTCACAGCC 72
54  GCGCCACAACGACGAGCTGCTGAGCGCATGCTGAGGGGAAATCACCACTTCACAGCC 113

73  TGCACGAGAGTTTAATCTGCTCTCCAGGGAAATTAAGAAGCCCAAACTCTCTACTGTA 132
114 TGACGAGAGTTTAATCTGCTCTCCAGGGAAATTAAGAAGCCCAAACTCTCTACTGTA 173

133 GCACCGGGGCCCATCTTCGAGGATCTCTCCGATGCACAGTGGATGGGACAGGACA 192
174 GCACCGGGGCCCATCTTCGAGGATCTCTCCGATGCACAGTGGATGGGACAGGACA 233

193 GGAGCGCACAGCAANTTACGTGCAGCTCAAGTSCGGAAGCGTGGGGGAGGTGTATATA 252
234 GGAGCGCACAGCAANTTACGTGCAGCTCAAGTSCGGAAGCGTGGGGGAGGTGTATATA 293

253 AGAGTACCGGAGCTGGCCAGTACTTGGCCATGCACACCGAGCGGCTTTATACGGCTCAC 312
294 AGAGTACCGGAGCTGGCCAGTACTTGGCCATGCACACCGAGCGGCTTTATACGGCTCAC 353

313 AGACACCAATGAGGAATGTT 333
354 AGACACCAATGAGGAATGTT 374

```

<b>RESULT 7</b>					
CD701495	522 bp	mRNA	linear	EST 25-JUN-2003	
EST18019 human nasopharynx Homo sapiens cDNA, mRNA sequence.					
DEFINITION	CD701495				
ACCESSION	CD701495.1	GI:32232125			
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 522)				
AUTHORS	Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.				
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 DongFeng Road East, Guangzhou 510060, China Tel.: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsums.edu.cn.				
FEATURES	Location/Qualifiers				
source	1..522				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/tissue_type="normal nasopharynx"				
	/clone_lib="human nasopharynx"				
	/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"				
<b>ORIGIN</b>					
Query Match	49.7%	Score 317;	DB 14;	Length 522;	
Best Local Similarity	100.0%;	Pred. No. 2.7e-151;			
Matches 317;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	13	GGCCCAACAGCAGCTGCTGAGCATGTGCAGAGGGGAATACCACCTTCACAGCCC	72		
Db	206	GGCCCCCAACAGCAGCTGCTGAGCCATGTGCTGAGGGGAATACCACCTTCACAGCCC	265		
QY	73	TGACCGAGAGTTTAATCTCCCTCCAGCGGAATTACAAGAGCCCAAACCTCTTACTTGTA	132		
Db	266	TGACCGAGAGTTTAACTCTCCCTCCAGCGGAATTACAAGAGCCCAAACCTCTTACTTGTA	325		
QY	133	GCACGGGGGCCCATCTTCTGAGAGTCTCTCCGAGTGGCACAGTGATGGACAGGGACA	192		
Db	326	GCACGGGGGGCCACTCTTCTGAGAGTCTCTCCGAGTGGCACAGTGATGGACAGGGACA	385		
QY	193	GGAGCGACAGCAGCATTCACGTGCGAGCTCAGTGCGBAAGCGTGGGGAGGTGTATATA	252		
Db	386	GGAGCGACAGCAGCATTCACGTGCGAGCTCAGTGCGBAAGCGTGGGGAGGTGTATATA	445		
QY	253	AGAGTAGCCGAGACTGGCCAGTACTTTGGCCATGGACACCGAGCGGCTTTATACGGCTCAC	312		
Db	446	AGAGTAGCCGAGACTGGCCAGTACTTTGGCCATGGACACCGAGCGGCTTTATACGGCTCAC	505		
QY	313	AGACACCAATGAGGAA	329		
Db	506	AGACACCAATGAGGAA	522		
<b>RESULT 8</b>					
SG706412	714 bp	mRNA	linear	EST 07-MAY-2001	
BG706412 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792378 5', mRNA sequence.					
DEFINITION	BG706412.1	GI:13981735			
ACCESSION	BG706412				
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 714)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cchapb-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10670 row: h column: 11  
High quality sequence stop: 710.  
Location/Qualifiers

FEATURES

source  
1. .714  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4792378"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC 96"  
/note="Organ: Brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI  
gtcagag); Oligo-dT primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.3 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC Library."

ORIGIN

Query Match 46.4%; Score 296; DB 12; Length 714;  
Best Local Similarity 99.7%; Pred. No. 1.7e-140;  
Matches 346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 100 GGAATTACAGAGAGCCCAACTCTCTACTGTAGCAACGCGGCGCCTCTCTGAGGATCC 159  
DB 210 GGATATACAGAGAGCCCAACTCTCTACTGTAGCAACGCGGCGCCTCTCTGAGGATCC 269  
QY 160 TTCGGAGTGCACAGTGGATGGAGCAAGGAGCAGAGCCAGCAGCAATTCAGCTGCAGC 219  
DB 270 TTCGGAGTGCACAGTGGATGGAGCAAGGAGCAGAGCCAGCAGCAATTCAGCTGCAGC 329  
QY 220 TCAGTCGGAGAGCGTGGGGAGGTGTATATAGATGACCGAGACTGGCCAGTCTGG 279  
DB 330 TCAGTCGGAGAGCGTGGGGAGGTGTATATAGATGACCGAGACTGGCCAGTCTGG 389  
QY 280 CCATGACACCGACGGGCTTTTATACGGCTCACAGACCAATAGGAATGTTTTC 339  
DB 390 CCATGACACCGACGGGCTTTTATACGGCTCACAGACCAATAGGAATGTTTTC 449  
QY 340 TGGAAAGGCTGGAGGAGACCACTTACACACCTATATCCAAAGAGCATGCGAGAGA 399  
DB 450 TGGAAAGGCTGGAGGAGACCACTTACACACCTATATCCAAAGAGCATGCGAGAGA 509  
QY 400 ATTGGTTTGTGGCTTCAAGAAGATGGGAGCTGCAACGCGGTCT 446  
DB 510 ATTGGTTTGTGGCTTCAAGAAGATGGGAGCTGCAACGCGGTCT 556

RESULT 9

BF956865  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
BF956865 461 bp mRNA linear EST 22-JAN-2001  
RC1-NN0233-221100-011-h12 NN0233 Homo sapiens cDNA, mRNA sequence.  
BF956865  
BF956865.1 GI:12374140  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 461)  
Dias Neto P., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,  
Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,  
Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H.,  
Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V.,

O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and  
Simpson A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
PUBMED  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-27049222  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gechtml2.pl?tl=RC1&t2=RC1-NN0233-221100-011-h12&t3=2000-11-22&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 11  
High quality sequence stop: 461.  
Location/Qualifiers

source  
1. .461  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NN0233"  
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (O.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

FEATURES

source  
1. .461  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NN0233"  
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (O.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

ORIGIN

Query Match 45.8%; Score 292; DB 10; Length 461;  
Best Local Similarity 100.0%; Pred. No. 1.8e-138;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 155 GATCCTTCCTCGGATGGCAGTGGATGGGACAGGAGCAGGACGACCACTTCAGCT 214  
DB 44 GATCCTTCCTCGGATGGCAGTGGATGGGACAGGAGCAGGACGACCACTTCAGCT 103  
QY 215 GCAGCTCAGTGGCGAAGCGTGGGGAGGTGTATATAGATGACCGAGCTGGCCAGTA 274  
DB 104 GCAGCTCAGTGGCGAAGCGTGGGGAGGTGTATATAGATGACCGAGCTGGCCAGTA 163  
QY 275 CTTCGCCATGACGACCGGCGCTTTTATACGGCTCACAGACCAATGAGGAATGTTT 334  
DB 164 CTTCGCCATGACGACCGGCGCTTTTATACGGCTCACAGACCAATGAGGAATGTTT 223  
QY 335 GTTCCTGGAAGGCTGGAGGAGACCACTTACACACCTATATCCAAAGAGCATGCGAGA 394  
DB 224 GTTCCTGGAAGGCTGGAGGAGACCACTTACACACCTATATCCAAAGAGCATGCGAGA 283  
QY 395 GAAGAAATGGTTTGTGGCTTCAAGAAGATGGGAGCTGCAACGCGGTCT 446  
DB 284 GAAGAAATGGTTTGTGGCTTCAAGAAGATGGGAGCTGCAACGCGGTCT 335

RESULT 10

BF953845  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
BF953845 878 bp mRNA linear EST 25-SEP-2001  
603027526F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5197783 5',  
mRNA sequence.  
BF953845  
BF953845.1 GI:15745423  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 878)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cga@rs-rcmail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11495 row: d column: 08  
High quality sequence stop: 703.  
Location/Qualifiers

## FEATURES

source

1. .878

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5197783"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: EcoRV (destroyed); RNA source anonymous pool of 6

male brains, age range 23-27 yo. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.5 kb. Insert size

range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 019. Note:

this is a NIH\_MGC Library."

## ORIGIN

Query Match 44.2%; Score 282; DB 12; Length 878;  
Best Local Similarity 100.0%; Pred. No. 2.8e-133;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 CTCCTCTACTGTGACACGGGGCGGCGCTTCCTGAGATCTTCGCGATCGCAGTGGAT 179

Db 199 CTCCTCTACTGTGACACGGGGCGGCGCTTCCTGAGATCTTCGCGATCGCAGTGGAT 258

QY 180 GGGACAGGGACAGGACGACGACCAATTCAGCTGAGCTGCGGAGAAAGCTGGGG 239

Db 259 GGGACAGGGACAGGACGACGACCAATTCAGCTGAGCTGCGGAGAAAGCTGGGG 318

QY 240 GAGGTGTATATTAAGAGTACCGAGCTGCGGAGTCTTGCCATGCGACCGCGGCTT 299

Db 319 GAGGTGTATATTAAGAGTACCGAGCTGCGGAGTCTTGCCATGCGACCGCGGCTT 378

QY 300 TTATACGGCTCACAGACCAATAGGAAATGTTGTTCTGAAAGCTGGAGGAC 359

Db 379 TTATACGGCTCACAGACCAATAGGAAATGTTGTTCTGAAAGCTGGAGGAC 438

QY 360 CATTACACACTTATATCCAGACGATCGACAGAGAT 401

Db 439 CATTACACACTTATATCCAGACGATCGACAGAGAT 480

## RESULT 11

BU840197

LOCUS

DEFINITION

AGENCOURT\_8964623 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:6379201

5', mRNA sequence.

ACCESSION

BU840197

VERSION

BU840197.1 GI:24024592

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 611)

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Agencourt

Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGTCACCTC. The cell lines was provided by Dr. James Martin from University of Iowa.

TAG: TISSUE=Enchondroma cell line (Mix of EN1 and EN2)  
TAG\_LIB=UI-H-FG0  
TAG\_SEQ=CCGTCACCTC

ORIGIN

Query Match 32.4%; Score 207; DB 13; Length 750;  
Best Local Similarity 100.0%; Pred. No. 8.9e-95;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 GAGGTGTATTAAGAGTACCGAGCTGGCCACTTGGCCATGACACACCGCGCTT 299  
DB 675 GAGGTGTATTAAGAGTACCGAGCTGGCCACTTGGCCATGACACACCGCGCTT 616  
QY 300 TTATACGGCTCACACACCAATGAGGAATGTTTGTCTGGAAGGCTGGAGGAGAC 359  
DB 615 TTATACGGCTCACACACCAATGAGGAATGTTTGTCTGGAAGGCTGGAGGAGAC 556  
QY 360 CATTACACACCTATATATCCAGAGCATGACAGAGAGATTTGTTTGGCTTCAAG 419  
DB 555 CATTACACACCTATATATCCAGAGCATGACAGAGAGATTTGTTTGGCTTCAAG 496  
QY 420 AAGATGGAGCTGCACAAACGGCTCT 446  
DB 495 AAGATGGAGCTGCACAAACGGCTCT 469

RESULT 14

AA015793 460 bp mRNA linear EST 29-NOV-1996  
LOCUS ze30a12.r1 Soares retina N2B4HR Homo sapiens cDNA clone  
DEFINITION IMAGE:360478 5' similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR  
PRECURSOR 1 (HUMAN); mRNA sequence.

ACCESSION AA015793  
VERSION AA015793.1 GI:1476960  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 460)  
REFERENCE Hillier, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, I., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
CONTACT: Wilson RK  
JOURNAL Washington University School of Medicine  
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert length: 3013 Std Error: 0.00  
Seq primer: -28M13 rev2 from Amerham  
High quality sequence stop: 372.  
Location/Qualifiers  
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/sex="male"  
/tissue\_type="retina"  
/dev\_stage="55 year old"  
/lab\_host="DH10B (ampicillin resistant)"

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert length: 3013 Std Error: 0.00  
Seq primer: -28M13 rev2 from Amerham  
High quality sequence stop: 372.  
Location/Qualifiers  
1. .460  
/organism="Homo sapiens"  
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/db\_xref="GDB:1277023"  
/db\_xref="taxon:9606"  
/clone="IMAGE:360478"  
/sex="male"  
/tissue\_type="retina"  
/dev\_stage="55 year old"  
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FEATURES  
source

source

1. .420  
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/note="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.9e-131;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGCCCAACAGCAGAGCTGCTGAGCCATGGCTGAAGGGGAATACACCTTCACAGCC 72  
DB 144 GCGCCCAACAGCAGAGCTGCTGAGCCATGGCTGAAGGGGAATACACCTTCACAGCC 203  
QY 73 TGACCGAAGTTTATCTGCTTCAGGGGATTAACAGAGCCCAAACTCTCTACTGTA 132  
DB 204 TGACCGAAGTTTATCTGCTTCAGGGGATTAACAGAGCCCAAACTCTCTACTGTA 263  
QY 133 GCACGGGGGCCACTTCTGAGGATCTTCGGGATGGCAGCTGGATGGGACAGGACA 192  
DB 264 GCACGGGGGCCACTTCTGAGGATCTTCGGGATGGCAGCTGGATGGGACAGGACA 323  
QY 193 GAGCGCAGCAGCAGCTGAGCTGAGCTGCGGAGAGCTGGGGAGGCTATATAA 252  
DB 324 GAGCGCAGCAGCAGCTGAGCTGAGCTGCGGAGAGCTGGGGAGGCTATATAA 383  
QY 253 AGATGACGAGCTGCGGAGAGCTGCGGAGAGCTGGGGAGGCTATATAA 289  
DB 384 AGATGACGAGCTGCGGAGAGCTGCGGAGAGCTGGGGAGGCTATATAA 420

RESULT 13

B0627243/c 750 bp mRNA linear EST 23-SEP-2002  
LOCUS UI-H-FG0-bct-n-05-0-UI.s1 NCI CGAP EN1.2 Homo sapiens cDNA clone  
DEFINITION UI-H-FG0-bct-n-05-0-UI 3', mRNA sequence.

ACCESSION B0627243  
VERSION B0627243.1 GI:23293457  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 750)  
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: James Martin  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu  
Seq primer: M13 FORWARD  
POLYA=Yes.  
Location/Qualifiers  
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/lab\_host="DH10B (Life Technologies)"  
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/note="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI CGAP EN1.2 is a cDNA library containing the following tissue(s): Enchondroma cell line (2 cell lines). The library was constructed according to Bonaldo, Lennon and

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: James Martin  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu  
Seq primer: M13 FORWARD  
POLYA=Yes.  
Location/Qualifiers  
1. .750  
/organism="Homo sapiens"  
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/clone="UI-H-FG0-bct-n-05-0-UI"  
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/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
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FEATURES  
source

/clone\_lib="Soares retina N2b4HR"  
 /notes="Organ: eye; Vector: pVT33 (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5,  
 5'-GTTTACCATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTT-3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pVT3 vector  
 (Pharmacia). The retinas were obtained from a 55 year old  
 Caucasian and total cellular poly(A)<sup>+</sup> RNA was extracted 6  
 hrs after their removal. The retina RNA was kindly  
 provided by Roderick R. McInnes M.D. Ph.D. from the  
 University of Toronto. Library constructed by Benito  
 Soares and M.Fátima Bonaído. "

## ORIGIN

Query Match	29.5%	Score 188	DB 12	Length 570
Best Local Similarity	100.0%	Pred. No. 4.8e-85		
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DB	124	GCSCCA	CAAGGAGCGAGCTGCTGAGCCATGGCTCAGAGGGAAATCACCACCTTCAGAGGCC	183
QY	73	TGACCG	GAGATTTAATCTGCTCTCAGGGAAATTACAGAGGCCCAAACTCCTCTACTGTA	132
DB	184	TGACCG	GAGATTTAATCTGCTCTCAGGGAAATTACAGAGGCCCAAACTCCTCTACTGTA	243
QY	133	GCAACGGGGGCC	ACTTCTCTGAGATCTCTTCGGATGGCAAGTGAGTGGAGCAGGGACA	192
DB	244	GCAACGGGGGCC	ACTTCTCTGAGATCTCTTCGGATGGCAAGTGAGTGGAGCAGGGACA	303
QY	193	GGAGCG	CAC 200	
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Job time : 2849 secs

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RESULT 15
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LOCUS      570 bp      mRNA      linear      EST 07-SEP-2001
DEFINITION 60324798f1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE15299508 5',
            mRNA sequence.

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ACCESSION	BI598882
VERSION	BI598882.1
	GI:15491821

**KEYWORDS**  
EST.  
**SOURCE**  
Homo sapiens (human)  
**ORGANISM**  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
**REFERENCE**  
1. (bases 1 to 570)  
**AUTHORS**  
NIH-MGC <http://mgc.ncbi.nih.gov/>.  
**TITLE**  
National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL**  
Unpublished (1999)  
**COMMENT**  
Contact: Robert Strausberg, Ph.D.

Email: csqabp-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Garincci (RIKEN)  
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC Clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LHAM11758 row: b column: 21  
High quality sequence stop: 570.

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FEATURES
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/lab_host="DH10B"
/clone_lib="NIH_MCC_96"
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insert size 2-3 kb and normalized to ROT 5. This is a

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Camugen Inc.  
ON protein - protein search, using sw model  
Run on: August 14, 2003, 10:21:43 ; Search time 41 Seconds  
US-10-022-54A-4  
536.192 Million cell updates/sec

Title:   
Sequences: 1. AEGITTFATLTKFNLPG.....PTHGQALFLFPLVSD 154  
Scoring cable: BLOSUM62  
Gapop 30.0 , Openat 0.5  
Searched: 1107863 seqs, 10972673 residues  
Total number of hits satisfying chosen parameters: 1107863  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 03  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the observed score.  
and is derived by analysis of the local score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	825	100.0	154	17	AA061805		Human beta-endothelial
2	825	100.0	154	17	AA061805		Human beta-endothelial
3	825	100.0	154	19	AA075414		Human beta-endothelial
4	825	100.0	154	20	AA092203		Human beta-endothelial
5	825	100.0	154	16	AA092203		Human beta-endothelial
6	825	100.0	155	16	AA094077		Human beta-endothelial
7	825	100.0	155	16	AA094077		Human beta-endothelial
8	825	100.0	155	16	AA094077		Human beta-endothelial
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11	825	100.0	155	19	AA053022		Human beta-endothelial
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18	825	100.0	155	22	AA050228		Human beta-endothelial
19	825	100.0	155	22	AA050228		Human beta-endothelial
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27	825	100.0	155	11	AA065785		Human beta-endothelial
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29	825	100.0	158	17	AA065785		Human beta-endothelial
30	825	100.0	158	17	AA065785		Human beta-endothelial
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37	825	100.0	158	17	AA065785		Human beta-endothelial
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40	825	100.0	158	17	AA065785		Human beta-endothelial
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ALIGNMENTS

Result 1  
AA065785  
ID AA065785 standard; Protein: 154 AA.  
XX  
AC AA065785

25-MAR-2003 (updated)  
17-MAR-1997 (first entry)  
XX Human endothelial cell growth factor-beta.  
XX Endothelial cell growth factor-beta, EGF-beta.  
XX Homo sapiens.  
XX US557390-A.  
XX 05-NOV-1995.  
XX 07-JUN-1995; 94US-047364.  
XX 18-DEC-1987; 87US-013499.  
XX 03-MAR-1986; 84US-083594.  
XX 22-MAR-1987; 85US-079859.  
XX 27-MAR-1991; 91US-079859.  
XX 03-NOV-1994; 94US-031484.  
XX 07-JUN-1995; 95US-047364.  
XX (ECHO) RHONE-POULENC ROGER PHARM INC.  
XX Burgess M., Drohan W., Jaye M., Maciej T.  
XX W01: 1996-555421/50.  
XX N-PDB: A74583.  
XX Recombinant human endothelial cell growth factors - for treating  
XX damaged blood vessels, etc.  
XX Claim 1: Column 16; 22pp; English.  
XX Human recombinant endothelial cell growth factors (ECGF) beta  
XX (AA065785) and alpha (AA065787) differ only at their N-terminal ends.  
XX They can be produced in transformed prokaryotic or eukaryotic host  
XX cells using DNA sequences (ATATTA and AATTA, respectively) derived  
XX from the cDNA sequences of human endothelial cells. The sequences of  
XX the EGFs are produced by culturing the host cells and recovering  
XX the proteins. EGFs have utility in the growth and amplification  
XX of endothelial cells in culture. They can potentially be used to  
XX treat endothelial dysfunction in atherosclerotic blood vessel  
XX structures, and also have diagnostic applications.  
XX (Updated on 25-MAR-2003 to correct PF field.)  
XX Sequence 154 AA.  
Query Match 100.0%; Score 825; DB 17; Length 154;  
Best Local Similarity 100.0%; Pred. No. 3.5e-44;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 SAEISGVVYKCTGQYLAQDTGLVSGQTNELFLERENNTTISPMEN 120  
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Db 121 MFVGLKNGSGSPRHQGLFLFPLVSD 154  
ID AA064805 standard; Protein: 154 AA.  
XX AA064805;  
XX 25-MAR-2003 (updated)  
XX 23-DEC-1996 (first entry)  
XX Human beta-endothelial cell growth factor.  
XX Endothelial cell growth factor; EGF; blood vessel; regeneration;  
XX Heparin-Sepharose affinity chromatography; probe; oligonucleotide;  
XX PF; fibroblast growth factor.  
XX Homo sapiens.  
XX US555328-A.  
XX 03-SEP-1994.  
XX 03-NOV-1994; 94US-031484.  
XX 18-DEC-1987; 87US-013499.  
XX 03-MAR-1986; 84US-083594.  
XX 27-MAR-1991; 91US-079859.  
XX 03-NOV-1994; 94US-031484.  
XX (ECHO) RHONE-POULENC ROGER PHARM INC.  
XX Burgess M., Maciej T.  
XX W01: 1996-43132/41.  
XX N-PDB: A73750.  
XX Isolated, purified, biologically active bovine beta endothelial cell  
XX growth factor - useful to regenerate or treat damaged blood vessels  
XX PF; fibroblast growth factor.  
XX Disclosure: Fig 6; 28pp; English.  
XX Bovine beta-endothelial cell growth factor (beta-EGF, AA065785) having  
XX a sequence identical to that of the beta-EGF isolated from bovine  
XX brain using Heparin-Sepharose affinity chromatography. EGF is  
XX useful for, among other purposes, diagnostic applications and has  
XX potential in the treatment of damaged blood vessels or other  
XX conditions associated with endothelial dysfunction.  
XX Human EGF (AA065785) or fragments may be obtained using  
XX oligonucleotides (AA065784 and AA065786) whose design is  
XX based on the sequence of bovine alpha- and beta-EGF.  
XX (Updated on 25-MAR-2003 to correct PF field.)  
XX Sequence 154 AA;







XX BI Burgess W, Drohan MN, Jays M, Maciej TJ;  
 XX WPI, 1994-154037/56.  
 XX MF52B, MV74136.  
 XX Compositions for promoting wound healing - containing endothelial  
 XX cell growth factor polypeptides  
 XX Example; Fig 8; 23pp; English.  
 XX This sequence represents the complete amino acid sequence of the human  
 XX endothelial cell growth factor (ECGF). The protein is further processed  
 XX to generate the beta-ECGF (starting from Ala at position 22: AM75413). When  
 XX and alpha-ECGF (starting from the Met at position 22: AM75413). When  
 XX the beta-ECGF is treated with a proteolytic enzyme, it is converted into  
 XX the alpha-ECGF. The sequence was isolated from a human brain stem cell cDNA  
 XX (a-PHF). The sequence was isolated from a human brain stem cell cDNA  
 XX library using a probe designed based on fragments of the bovine ECGF  
 XX (see AM75413 and 15414). The ECGF protein was used in the compositions for  
 XX cell growth factor polypeptides. ECGF is also used to give cells on a  
 XX prosthetic device.  
 XX Sequence 155 AA:  
 XX  
 XX Query Match 100.0%; Score 425; DB 19; Length 155;  
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-84;  
 XX Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 XX 1 ARGEITTTATKPLPONTKPKLLVCSNGHFLPDTVTNTRSHQIQGL 60  
 XX 2 ARGEITTTATKPLPONTKPKLLVCSNGHFLPDTVTNTRSHQIQGL 61  
 XX 61 SASVGVVITSTQVLAQMDGLVGSQTNKCLFLKLENNNTYISKDAEN 120  
 XX 62 SASVGVVITSTQVLAQMDGLVGSQTNKCLFLKLENNNTYISKDAEN 121  
 XX 121 MFVLKNSGSGPHTHYQVQALFLPVSVD 154  
 XX 122 MFVLKNSGSGPHTHYQVQALFLPVSVD 155  
 XX  
 XX RESULT 10  
 XX AM75711 standard; Protein: 155 AA.  
 XX AC AM75711;  
 XX 05-AUG-1998; (first entry)  
 XX Fibroblast growth factor-1.  
 XX Fibroblast growth factor-1. Pgf-1, murine; protein engineering;  
 XX heparin; thrombosis; thrombolytic; thrombolytic; thrombolytic;  
 XX human; thrombosis.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Misc-difference 100  
 XX /note: "Phe-100 is replaced by another amino acid  
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 XX Gly, Met, Leu or Tyr, especially Ala, Gly  
 XX or Ser"  
 XX Misc-difference 102  
 XX /note: "Gln-102 may be replaced by another amino  
 XX acid (Claim 7). Preferably Ala, Gly or Ser"  
 XX Misc-difference 107  
 XX /note: "Ala-107 may be replaced by another amino  
 XX acid (Claim 2). Preferably Ala, Phe, Ser,  
 XX Gly, Met, Leu or Tyr, especially Ala, Gly  
 XX or Ser"  
 XX Misc-difference 110  
 XX /note: "Asn-110 may be replaced by another amino  
 XX acid (Claim 1). Preferably Ala, Phe, Ser,  
 XX Gly, Met, Leu or Tyr, especially Ala, Gly  
 XX or Ser"  
 XX WC9339436-A2.  
 XX 11-SEP-1998.  
 XX 03-MAR-1998; 98MO-760078.  
 XX 03-MAR-1997; 97US-0640765.  
 XX (HSA) EIGAL CO LTD.  
 XX Kalyanaswami R, Kawai T, Zhu M;  
 XX WPI, 1996-495643/42.  
 XX Fibroblast growth factor protein and DNA - having reduced receptor  
 XX binding and able to bind heparin, useful for treating and regulating  
 XX heparin-related disorders e.g. thrombosis  
 XX Disclosure; Page 52; 71pp; English.  
 XX This is the amino acid sequence of fibroblast growth factor-1  
 XX (FGF-1). Claimed DNA molecules of the invention encode FGF protein  
 XX having reduced receptor binding activity but retain the ability to bind heparin. For FGF-1,  
 XX amino acid residues 100, 107 or 110 are preferably replaced by  
 XX other amino acid residues, with an optional further replacement of  
 XX residue 102. The amino acid sequence may be substituted with a  
 XX replacement of the Cys residues to reduce receptor binding. The protein  
 XX is obtained by site-specific or site-directed mutagenesis of FGF-1  
 XX cDNA. Incorporation of the mutated DNA into a vector and expression  
 XX in host cells. The FGF protein are used to treat heparin-related  
 XX disorders and heparin-related disorders. The protein is used to treat  
 XX thrombosis and heparin-associated thrombocytopenia and  
 XX thrombosis. They may also be used for drug design.  
 XX Sequence 155 AA:  
 XX  
 XX Query Match 100.0%; Score 425; DB 19; Length 155;  
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-84;  
 XX Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 ARGEITTTATKPLPONTKPKLLVCSNGHFLPDTVTNTRSHQIQGL 60  
 XX 2 ARGEITTTATKPLPONTKPKLLVCSNGHFLPDTVTNTRSHQIQGL 61  
 XX 61 SASVGVVITSTQVLAQMDGLVGSQTNKCLFLKLENNNTYISKDAEN 120  
 XX 62 SASVGVVITSTQVLAQMDGLVGSQTNKCLFLKLENNNTYISKDAEN 121  
 XX 121 MFVLKNSGSGPHTHYQVQALFLPVSVD 154  
 XX 122 MFVLKNSGSGPHTHYQVQALFLPVSVD 155  
 XX  
 XX RESULT 12  
 XX AM75554 standard; Protein: 155 AA.  
 XX AC AM75554;  
 XX 05-AUG-1998; (first entry)  
 XX Human Pgf-1 protein fragment.  
 XX PFG-1; PFG-19, fibroblast growth factor; human; diagnosis; treatment;  
 XX tumor; neoplastic cell growth; cell proliferation; tumorigenesis; cancer;  
 XX autocrine signalling; Pgf-1.  
 XX Homo sapiens.  
 XX WC9327100-A1.  
 XX 03-JUN-1999.  
 XX 25-NOV-1998; 98MO-0252190.  
 XX 21-SEP-1998; 98US-0554432.  
 XX 25-AUG-1997; 97US-0606461.  
 XX (HSA) GENENTEC INC.  
 XX Borestein D, Golder A, Gurney AL, Hillan KJ, Lawrence DA;  
 XX WPI, 1999-347711/29.  
 XX Nucleic acid encoding fibroblast growth factor - 19, useful for the  
 XX diagnosis, prevention and treatment of cancer  
 XX Disclosure; Fig 11; 85pp; English.  
 XX This invention describes a novel human fibroblast growth factor, PFG533,  
 XX also known as fibroblast growth factor-19 (PFG-19). The nucleic acid,  
 XX protein, polypeptide, and/or gene encoding the protein, polypeptide,  
 XX and/or gene of human fibroblast growth factor-19, characterized by modulation of  
 XX PFG533 expression, or in the preparation of compositions for such

QY 1 ARGEITTTATKPLPONTKPKLLVCSNGHFLPDTVTNTRSHQIQGL 60  
 DB 2 ARGEITTTATKPLPONTKPKLLVCSNGHFLPDTVTNTRSHQIQGL 61  
 QY 61 SASVGVVITSTQVLAQMDGLVGSQTNKCLFLKLENNNTYISKDAEN 120  
 DB 62 SASVGVVITSTQVLAQMDGLVGSQTNKCLFLKLENNNTYISKDAEN 121  
 QY 121 MFVLKNSGSGPHTHYQVQALFLPVSVD 154  
 DB 122 MFVLKNSGSGPHTHYQVQALFLPVSVD 155  
 XX  
 XX RESULT 11  
 XX AM75302 standard; Protein: 155 AA.  
 XX AC AM75302;  
 XX 14-AUG-1998; (first entry)  
 XX Fibroblast growth factor protein 1.  
 XX Pgf, cell growth; survival; differentiation; central nervous system;  
 XX peripheral nervous tissue; treatment; diagnosis; cell culture.  
 XX Mammalian.  
 XX WC938864-A1.  
 XX 05-MAR-1998.  
 XX 27-AUG-1997; 97MO-0513237.  
 XX 30-AUG-1996; 96US-070245.  
 XX (HSA) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX Natkams J, Smallwood PW;  
 XX WPI, 1998-179380/16.  
 XX New fibroblast growth factor homologous factors - useful for, e.g.  
 XX treatment of neurodegenerative and neoplastic disorders  
 XX Disclosure; Page 50-51; 94pp; English.  
 XX Fibroblast growth factor (FGF) proteins (AM75302-W31024 and  
 XX AM75302-W31033) are members of the fibroblast growth factor family and  
 XX have homology to fibroblast growth factor homologous factor (FGF)  
 XX which is a secreted protein that stimulates cell growth and survival.  
 XX growth, survival, and differentiation of cells in the central nervous  
 XX system, as well as cells in peripheral nervous tissue. The proteins can  
 XX therefore be used for treating and diagnosing conditions involving the  
 XX central nervous system. The proteins can also be used for promoting  
 XX cultured cells or tissues or to promote neuron growth in vitro.  
 XX Sequence 155 AA:  
 XX  
 XX Query Match 100.0%; Score 425; DB 19; Length 155;  
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-84;  
 XX Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 ARGEITTTATKPLPONTKPKLLVCSNGHFLPDTVTNTRSHQIQGL 60  
 XX 2 ARGEITTTATKPLPONTKPKLLVCSNGHFLPDTVTNTRSHQIQGL 61  
 XX 61 SASVGVVITSTQVLAQMDGLVGSQTNKCLFLKLENNNTYISKDAEN 120  
 XX 62 SASVGVVITSTQVLAQMDGLVGSQTNKCLFLKLENNNTYISKDAEN 121  
 XX 121 MFVLKNSGSGPHTHYQVQALFLPVSVD 154  
 XX 122 MFVLKNSGSGPHTHYQVQALFLPVSVD 155  
 XX  
 XX RESULT 12  
 XX AM75554 standard; Protein: 155 AA.  
 XX AC AM75554;  
 XX 05-AUG-1998; (first entry)  
 XX Human Pgf-1 protein fragment.  
 XX PFG-1; PFG-19, fibroblast growth factor; human; diagnosis; treatment;  
 XX tumor; neoplastic cell growth; cell proliferation; tumorigenesis; cancer;  
 XX autocrine signalling; Pgf-1.  
 XX Homo sapiens.  
 XX WC9327100-A1.  
 XX 03-JUN-1999.  
 XX 25-NOV-1998; 98MO-0252190.  
 XX 21-SEP-1998; 98US-0554432.  
 XX 25-AUG-1997; 97US-0606461.  
 XX (HSA) GENENTEC INC.  
 XX Borestein D, Golder A, Gurney AL, Hillan KJ, Lawrence DA;  
 XX WPI, 1999-347711/29.  
 XX Nucleic acid encoding fibroblast growth factor - 19, useful for the  
 XX diagnosis, prevention and treatment of cancer  
 XX Disclosure; Fig 11; 85pp; English.  
 XX This invention describes a novel human fibroblast growth factor, PFG533,  
 XX also known as fibroblast growth factor-19 (PFG-19). The nucleic acid,  
 XX protein, polypeptide, and/or gene encoding the protein, polypeptide,  
 XX and/or gene of human fibroblast growth factor-19, characterized by modulation of  
 XX PFG533 expression, or in the preparation of compositions for such







DB 2 ABSEITTTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 61  
QY 61 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 120  
DB 62 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 121  
QY 121 WYGLKNSKSGRPHNTOQALFLPVSSED 154  
DB 122 WYGLKNSKSGRPHNTOQALFLPVSSED 155

RESULT 7  
US-09-103-079-9  
Sequence 9, Application US/09103079A  
Patent No. 6014775  
INVENTOR: J. Andrew  
APPLICANT: Greene, John M.  
TITLE OF INVENTION: Fibroblast Growth Factor 15  
CURRENT FILING DATE: US/09103079A  
EARLIER APPLICATION NUMBER: US/09103079A  
SEQUENCE CHARACTERISTICS:  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 9  
ORGANISM: Homo sapiens  
TYPE: PRT  
FEATURES:  
US-09-103-079-9

Query Match 100.0%; Score 825; DB 3; Length 155;  
Best Local Similarity 100.0%; Pred. No. 3.1e-87;  
Matches 154; Conservative 0; Mismatch 0; Indels 0; Gaps 0;  
QY 1 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 60  
DB 2 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 61  
QY 61 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 120  
DB 62 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 121  
QY 121 WYGLKNSKSGRPHNTOQALFLPVSSED 154  
DB 122 WYGLKNSKSGRPHNTOQALFLPVSSED 155

RESULT 8  
US-08-705-245-5  
Sequence 10, Application US/08705245  
Patent No. 620189  
INVENTOR: Nathanael et al., Jeremy  
APPLICANT: Nathanael et al., Jeremy  
TITLE OF INVENTION: FACTORS (FRA) AND METHODS OF USE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 06/06/95, 245  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Nathanael et al., Jeremy  
REGISTRATION NUMBER: 07165/094001  
REFERENCE/DOCKET NUMBER:  
TELEPHONE: 619/671-5959  
TELEFAX: 619/671-5959  
INFORMATION FOR SEQ ID NO: 5;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 amino acids  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: linear  
US-08-705-245-5

Query Match 100.0%; Score 825; DB 3; Length 155;  
Best Local Similarity 100.0%; Pred. No. 3.1e-87;  
Matches 154; Conservative 0; Mismatch 0; Indels 0; Gaps 0;  
QY 1 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 60  
DB 2 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 61  
QY 61 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 120  
DB 62 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 121  
QY 121 WYGLKNSKSGRPHNTOQALFLPVSSED 154  
DB 122 WYGLKNSKSGRPHNTOQALFLPVSSED 155

RESULT 9  
US-08-716-904-10  
Sequence 10, Application US/08716904  
Patent No. 603329  
INVENTOR: J. Andrew  
APPLICANT: Chaudhri, Louis Ann  
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP  
STREET: 8100 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 04-SEP-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SEED and BERRY LLP  
REGISTRATION NUMBER: 39-317  
REFERENCE/DOCKET NUMBER: 60100-415C1  
TELEPHONE: (206) 422-4900  
TELEFAX: (206) 422-4900  
INFORMATION FOR SEQ ID NO: 10;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLUCULE TYPE: peptide  
FEATURES:  
US-08-716-904-10

Query Match 100.0%; Score 825; DB 3; Length 155;  
Best Local Similarity 100.0%; Pred. No. 3.1e-87;  
Matches 154; Conservative 0; Mismatch 0; Indels 0; Gaps 0;  
QY 1 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 60  
DB 2 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 61  
QY 61 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 120  
DB 62 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 121  
QY 121 WYGLKNSKSGRPHNTOQALFLPVSSED 154  
DB 122 WYGLKNSKSGRPHNTOQALFLPVSSED 155

RESULT 10  
US-08-702-455-9  
Sequence 15, Application US/0802452A  
Patent No. 6077692  
INVENTOR: STEURM M.  
APPLICANT: STEURM M.  
TITLE OF INVENTION: FACTORS (FRA) AND METHODS OF USE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 06/06/95, 245  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Nathanael et al., Jeremy  
REGISTRATION NUMBER: 07165/094001  
REFERENCE/DOCKET NUMBER:  
TELEPHONE: 619/671-5959  
TELEFAX: 619/671-5959  
INFORMATION FOR SEQ ID NO: 5;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 amino acids  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: linear  
US-08-702-455-9

Query Match 100.0%; Score 825; DB 3; Length 155;  
Best Local Similarity 100.0%; Pred. No. 3.1e-87;  
Matches 154; Conservative 0; Mismatch 0; Indels 0; Gaps 0;  
QY 1 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 60  
DB 2 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 61  
QY 61 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 120  
DB 62 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 121  
QY 121 WYGLKNSKSGRPHNTOQALFLPVSSED 154  
DB 122 WYGLKNSKSGRPHNTOQALFLPVSSED 155

RESULT 11  
US-08-702-445-5  
Sequence 15, Application US/0802445A  
Patent No. 6077692  
INVENTOR: STEURM M.  
APPLICANT: STEURM M.  
TITLE OF INVENTION: FACTORS (FRA) AND METHODS OF USE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 06/06/95, 245  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Nathanael et al., Jeremy  
REGISTRATION NUMBER: 07165/094001  
REFERENCE/DOCKET NUMBER:  
TELEPHONE: 619/671-5959  
TELEFAX: 619/671-5959  
INFORMATION FOR SEQ ID NO: 5;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 amino acids  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: linear  
US-08-702-445-5

Query Match 100.0%; Score 825; DB 3; Length 155;  
Best Local Similarity 100.0%; Pred. No. 3.1e-87;  
Matches 154; Conservative 0; Mismatch 0; Indels 0; Gaps 0;  
QY 1 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 60  
DB 2 ABSEITTTALTRFPPONTKFFKLLVCNNGHFAILPDTOTVOTRUBSDHQLOQ 61  
QY 61 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 120  
DB 62 SASVGVVIVSTQVLANCUTGOLLSQTSOTRSCFLERLENNNTTISKAKEN 121  
QY 121 WYGLKNSKSGRPHNTOQALFLPVSSED 154  
DB 122 WYGLKNSKSGRPHNTOQALFLPVSSED 155

RESULT 12  
US-08-716-904-10  
Sequence 10, Application US/08716904  
Patent No. 603329  
INVENTOR: J. Andrew  
APPLICANT: Chaudhri, Louis Ann  
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:



US-09-449-249-10

Query Match 100.0%; Score 825; DB 4; Length 154;  
Best Local Similarity 100.0%; Pred. No. 4; Length 154;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGGTTTATLTKFNPNTKPKKLYCSNGHFLPDTVOOTRUSQHQIQ 60  
DB 2 ASGGTTTATLTKFNPNTKPKKLYCSNGHFLPDTVOOTRUSQHQIQ 60

QY 61 SASVGVYVSTKTVQGLAMTGLLYGSGTNECLFLERLNNNTYISKRAEN 120  
DB 62 SASVGVYVSTKTVQGLAMTGLLYGSGTNECLFLERLNNNTYISKRAEN 120

QY 121 MPVLKNSCKRGPHTHQVQLLPLFVPSD 154  
DB 122 MPVLKNSCKRGPHTHQVQLLPLFVPSD 154

Search completed: August 14, 2003, 10:28:04  
Job time : 19 sec

GenCode version 5.1.6  
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OM protein - protein search, using w model

Run on: August 14, 2003, 10:27:24 ; Search time 56 Seconds  
Maximum DB seq length: 360,259 Million cell updates/sec

Title: US-10-022-554A-4  
Sequence: 2 ASGGTTTATLTKFNPNTKPKKLYCSNGHFLPDTVOOTRUSQHQIQ 60

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 492763 seqs, 11002157 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0  
Maximum DB seq length: 36000050  
Post-processing: Minimum Match 0%

Listing first 45 summaries

Database 1: Published Applications A1:  
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2: /cpn2\_5/prodatea1/pubpa/US09\_PUBCOMB.pep\*  
3: /cpn2\_5/prodatea1/pubpa/US09\_PUBCOMB.pep\*  
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9: /cpn2\_5/prodatea1/pubpa/US09\_PUBCOMB.pep\*  
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16: /cpn2\_5/prodatea1/pubpa/US09\_PUBCOMB.pep\*  
17: /cpn2\_5/prodatea1/pubpa/US09\_PUBCOMB.pep\*  
18: /cpn2\_5/prodatea1/pubpa/US09\_PUBCOMB.pep\*

ALIGNMENTS

RESULT 1  
US-09-449-249-10  
Patent No. US090205522A1  
GENERAL INFORMATION:  
APPLICANT: Stepanov, Thomas  
INVENTOR: Stepanov, Thomas  
APPLICANT: Chernykh, Svetlana I.  
INVENTOR: Chernykh, Svetlana I.  
APPLICANT: Slavchenko, Iryna Yu.  
INVENTOR: Slavchenko, Iryna Yu.  
FILE REFERENCE: CYBENG 008A  
CURRENT APPLICATION NUMBER: US/09/529,945  
PRIORITY DATE: 2003-09-15  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 8  
SEQUENCE LENGTH: 154  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-449-249-10

Query Match 100.0%; Score 825; DB 10; Length 154;  
Best Local Similarity 100.0%; Pred. No. 4; Length 154;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGGTTTATLTKFNPNTKPKKLYCSNGHFLPDTVOOTRUSQHQIQ 60  
DB 1 ASGGTTTATLTKFNPNTKPKKLYCSNGHFLPDTVOOTRUSQHQIQ 60

QY 61 SASVGVYVSTKTVQGLAMTGLLYGSGTNECLFLERLNNNTYISKRAEN 120  
DB 61 SASVGVYVSTKTVQGLAMTGLLYGSGTNECLFLERLNNNTYISKRAEN 120

QY 121 MPVLKNSCKRGPHTHQVQLLPLFVPSD 154  
DB 121 MPVLKNSCKRGPHTHQVQLLPLFVPSD 154

RESULT 2  
US-10-022-554A-4  
Patent No. US090205522A1  
GENERAL INFORMATION:  
APPLICANT: Stepanov, Thomas  
INVENTOR: Stepanov, Thomas  
APPLICANT: Chernykh, Svetlana I.  
INVENTOR: Chernykh, Svetlana I.  
APPLICANT: Slavchenko, Iryna Yu.  
INVENTOR: Slavchenko, Iryna Yu.  
FILE REFERENCE: CYBENG 008A  
CURRENT APPLICATION NUMBER: US/09/529,945  
PRIORITY DATE: 2003-09-15  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 8  
SEQUENCE LENGTH: 154  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-022-554A-4

Query Match 100.0%; Score 825; DB 15; Length 154;  
Best Local Similarity 100.0%; Pred. No. 4; Length 154;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGGTTTATLTKFNPNTKPKKLYCSNGHFLPDTVOOTRUSQHQIQ 60  
DB 1 ASGGTTTATLTKFNPNTKPKKLYCSNGHFLPDTVOOTRUSQHQIQ 60

QY 61 SASVGVYVSTKTVQGLAMTGLLYGSGTNECLFLERLNNNTYISKRAEN 120  
DB 61 SASVGVYVSTKTVQGLAMTGLLYGSGTNECLFLERLNNNTYISKRAEN 120

SUMMARIES

Result 8  
No. Score Match Length DB ID Description  
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2 825 100.0 154 10 US-09-449-249-10 Sequence 8, Appl  
3 825 100.0 155 9 US-09-244-662A-3 Sequence 8, Appl  
4 825 100.0 155 9 US-09-244-662A-3 Sequence 8, Appl  
5 825 100.0 155 9 US-09-244-662A-3 Sequence 8, Appl



DB 61 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 120  
QY 121 WFLVKNKSCGKPTTHQQAILEFPVSD 154  
DB 121 WFLVKNKSCGKPTTHQQAILEFPVSD 154

RESULT 3

US-09-284-663A-9  
Sequence 9, Application US/0928463A  
Patent No. US2002013961A1  
GENERAL INFORMATION:  
APPLICANT: Borsacini, David A.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Lawrence, David A.  
APPLICANT: Roy, Margaret Ann  
TITLE OF INVENTION: Fibroblast Growth Factor-19  
CURRENT APPLICATION NUMBER: US/09/284,63A  
CURRENT FILING DATE: 1999-04-15  
NUMBER OF SEQ ID NOS: 30  
SEQ ID NO 1  
SEQ ID NO 2  
SEQ ID NO 3  
LENGTH: 155  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-284-663A-9

Query Match 100.0%; Score 825; DB 9; Length 155;  
Best Local Similarity 100.0%; Pred. No. 4.1e-84;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 60  
DB 2 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 61  
QY 61 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 120  
DB 62 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 121  
QY 121 WFLVKNKSCGKPTTHQQAILEFPVSD 154  
DB 122 WFLVKNKSCGKPTTHQQAILEFPVSD 155

RESULT 4

US-09-902-773A-3  
Sequence 9, Application US/0902773A  
Patent No. US20020034781A1  
GENERAL INFORMATION:  
APPLICANT: JUNG, SHAN  
APPLICANT: DOCAVON, JEANINE D.  
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-10  
NUMBER OF SEQUENCES: 14  
CORRESPONDING SEQ ID NOS: 1-14  
COMPOSER: STRONG  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-1914  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release 81.0, Version 81.30  
CURRENT APPLICATION DATA: US/09/902,773A  
FILING DATE: 12 Jul-2001  
CLASSIFICATION: Unknown  
PRIORITY APPLICATION DATA: US/08/803,926  
FILING DATE: 21 FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: STRONG, A. K.  
REFERENCE/DOCKET NUMBER: 1488-0350001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE (303) 371-2400  
TELEFAX (303) 371-2544  
INFORMATION FOR SEQ ID NO: 3  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: SHG ID NO. 3:  
US-09-902-773A-3

Query Match 100.0%; Score 825; DB 9; Length 155;  
Best Local Similarity 100.0%; Pred. No. 4.1e-84;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 60  
DB 2 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 61  
QY 61 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 120  
DB 62 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 121  
QY 121 WFLVKNKSCGKPTTHQQAILEFPVSD 154  
DB 122 WFLVKNKSCGKPTTHQQAILEFPVSD 155

RESULT 5

US-09-284-663A-9  
Sequence 9, Application US/0928463A  
Patent No. US2002013961A1  
GENERAL INFORMATION:  
APPLICANT: Borsacini, David A.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Lawrence, David A.  
APPLICANT: Roy, Margaret Ann  
TITLE OF INVENTION: Fibroblast Growth Factor-19  
CURRENT APPLICATION NUMBER: US/09/284,63A  
CURRENT FILING DATE: 1999-04-15  
NUMBER OF SEQ ID NOS: 30  
SEQ ID NO 1  
SEQ ID NO 2  
SEQ ID NO 3  
LENGTH: 155  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-284-663A-9

FILE REFERENCE: 07265/047003  
CURRENT APPLICATION NUMBER: US/09/251,263  
CURRENT FILING DATE: 1997-06-02  
EARLIER APPLICATION NUMBER: 08/867,471  
EARLIER FILING DATE: 1997-06-02  
CORRESPONDING SEQ ID NOS: 1-12  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
SEQ ID NO 10  
SEQ ID NO 11  
LENGTH: 155  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-251-263-9

Query Match 100.0%; Score 825; DB 9; Length 155;  
Best Local Similarity 100.0%; Pred. No. 4.1e-84;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 60  
DB 2 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 61  
QY 61 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 120  
DB 62 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 121  
QY 121 WFLVKNKSCGKPTTHQQAILEFPVSD 154  
DB 122 WFLVKNKSCGKPTTHQQAILEFPVSD 155

RESULT 6

US-09-425-021-9  
Sequence 9, Application US/09425021  
Patent No. US2002007674A1  
GENERAL INFORMATION:  
APPLICANT: Koseci, Chris A.  
APPLICANT: Koseci, John M.  
TITLE OF INVENTION: Fibroblast Growth Factor 15  
CURRENT APPLICATION NUMBER: US/09/425,021  
CURRENT FILING DATE: 1999-12-25  
EARLIER APPLICATION NUMBER: US/00/03,079  
EARLIER FILING DATE: 1998-06-23  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 1  
SEQ ID NO 2  
LENGTH: 155  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-425-021-9

Query Match 100.0%; Score 825; DB 9; Length 155;  
Best Local Similarity 100.0%; Pred. No. 4.1e-84;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 60  
DB 2 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 61  
QY 61 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 120  
DB 62 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 121  
QY 121 WFLVKNKSCGKPTTHQQAILEFPVSD 154  
DB 122 WFLVKNKSCGKPTTHQQAILEFPVSD 155

RESULT 7

US-09-249-918-2  
Sequence 2, Application US/09249918  
Patent No. US2002005678A1  
GENERAL INFORMATION:  
APPLICANT: Vucelja, J.  
APPLICANT: Kozlovskiy, Alexander I.  
APPLICANT: Chernykh, Svetlana I.  
APPLICANT: Slavchenko, Irina Yu.  
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDES  
FILE REFERENCE: PHAGE 006A  
CURRENT APPLICATION NUMBER: US/09/249,918  
CURRENT FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 09/318,288  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
SEQ ID NO 2  
LENGTH: 155  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-249-918-2

Query Match 100.0%; Score 825; DB 9; Length 155;  
Best Local Similarity 100.0%; Pred. No. 4.1e-84;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 60  
DB 2 ARGGTTTATCTGPPGKPKKLLVCSGNGHFLIPDPTVGTNRSGHQLQGL 61  
QY 61 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 120  
DB 62 SAEVGVVYKSTQVLAUTDGLVSGTNECFLENNNTYISKAREN 121  
QY 121 WFLVKNKSCGKPTTHQQAILEFPVSD 154  
DB 122 WFLVKNKSCGKPTTHQQAILEFPVSD 155

RESULT 8

US-09-249-918-11  
Sequence 11, Application US/09249918  
Patent No. US2002005678A1  
GENERAL INFORMATION:  
APPLICANT: Vucelja, J.  
APPLICANT: Kozlovskiy, Alexander I.  
APPLICANT: Chernykh, Svetlana I.  
APPLICANT: Slavchenko, Irina Yu.  
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDES  
FILE REFERENCE: PHAGE 006A  
CURRENT APPLICATION NUMBER: US/09/249,918  
CURRENT FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 09/318,288  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
SEQ ID NO 2  
LENGTH: 155  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-249-918-11



```

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 155
ORGANISM: Homo sapiens
US-10-075-445-2

Query Match 100.0% Score 825; DM 15; Length 155;
Best Local Similarity 100.0%; Fwd. No. 4,1e-84;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0

GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN N.
STERNER, PABLO
BARRY, MARK A.
MEURICK, DONNA
ZHANG, JUN
MOORE, PAUL A.
COLEMAN, TIMOTHY A.
GRUBER, JOACHIM R.
TITLE OF INVENTION: A METHOD FOR MONITORING GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESSES:
ADDRESS: STORKE, KESSLER, GOLUSTEIN & FOX, P.C.I.C.
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent Release 81.0, Version 81.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US7/10/075,446
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/461,158
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 62/023,852
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: US 60/039,045
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: US 60/025,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,688
REFERENCE/DOCET NUMBER: 1488, 030008/RFS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO 16:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
SEQUENCE DESCRIPTION:
STRANDNESS: NO. US203032667AT Relevant
TOPOLGY: NO. US203032667AT Relevant
MOL. WEIGHT: 155
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-075-445-16

Query Match 100.0%; Score 825; DM 16; Length 155;
Best Local Similarity 100.0%; Fwd. No. 4,1e-84;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 AGRSTPTATATKPLKPNPTKPKKPLKLVCSNGQHPARLPDPTQVTRKSDQGL 60
Db 2 AGRSTPTATATKPLKPNPTKPKKPLKLVCSNGQHPARLPDPTQVTRKSDQGL 61
Qy 61 SASRQVSVYKSTETQVLTQGLVQSGTQMGKGLPELRNNVNTYISKRAEN 120
Db 62 SASRQVSVYKSTETQVLTQGLVQSGTQMGKGLPELRNNVNTYISKRAEN 121
Qy 121 MYFLKLNKSCSGPRPTQGGALILFLPVPSSD 154
Db 122 MYFLKLNKSCSGPRPTQGGALILFLPVPSSD 155

RESULT 15
US-10-075-446-16
Sequence 16, Application US7/10075446
Fwd. No. 4,1e-84;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN N.
STERNER, PABLO
BARRY, MARK A.
MEURICK, DONNA
ZHANG, JUN
MOORE, PAUL A.
COLEMAN, TIMOTHY A.
GRUBER, JOACHIM R.
TITLE OF INVENTION: A METHOD FOR MONITORING GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESSES:
ADDRESS: STORKE, KESSLER, GOLUSTEIN & FOX, P.C.I.C.
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent Release 81.0, Version 81.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US7/10/075,446
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/461,158
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 62/023,852
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: US 60/039,045
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: US 60/025,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,688
REFERENCE/DOCET NUMBER: 1488, 030008/RFS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO 16:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
SEQUENCE DESCRIPTION:
STRANDNESS: NO. US203032667AT Relevant
TOPOLGY: NO. US203032667AT Relevant
MOL. WEIGHT: 155
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-075-446-16

Search completed: August 14, 2003, 10:35:59
Job time : 57 sec

Copyright (C) 1993 - 2003 CompuGen Inc.
GenCode version 5.1.6
August 14, 2003, 10:34:58 : Search time 19 Seconds
(Run on) (without alignments)
OM protein - protein search, using sw model

```





[illegible]

[illegible]







[illegible][illegible]

[illegible]

RESULT 6  
FGF1 CHYCI

[illegible]

OS Eukarya; eukaryotes; Metazoa; Chordata; Vertebrata; Butelelalomoni;  
OC Mammalia; Buthria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OC Ovis montanus.  
CC (1)  
RP SEQUENCE FROM N.A.  
RP Saitou N., Mond A.W., Raphael K.A., Cui G.R.:  
RN Annotation (SRA-254) on the OMNI/GenBank/EMBL databases.  
RN (2)  
RP SEQUENCE OF 9-155  
KA MEDLINE: 93245597; PubMed: 1674466;  
DR PROBLEM: P000483; ID: UNP0F:  
DR PRINTS: PR00242; ILIH0GF.  
AT Rubus A.K., Burgess A.M.; Lloyd C.J., Pabst L.J., Nice E.C.:  
RT Primary structure of ovine placental basic fibroblast growth  
CC factor.  
CC FEEL: 224-128-132(134NT).  
CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS  
CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN  
CC CONCENTRATION RANGE 5-100 NG/ML. THESE GROWTH FACTORS  
CC -1- SUBUNIT: MONOMER.  
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES  
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
CC The SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC CC by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>).  
CC DR PMR: L26136; AAA15113.1.-.  
DR MSP: P00018; UNP0F:  
DR PRINTS: PR00242; ILIH0GF.  
DR PROBLEM: P000483; ID: UNP0F:  
DR PRINTS: PR00242; ILIH0GF.  
DR PROSITE: PS00247; HB0F; 1.  
GM Growth Factor; Mitogen; Angiogenesis; Hepatic-binding.  
FT PROPEP 1 315 9 HEPARIN-BINDING GROWTH FACTOR 2.  
FT SITE 45 48 CELL ATTACHMENT SITE (POTENTIAL).  
FT SITE 87 90 CELL ATTACHMENT SITE (POTENTIAL).  
FT RESIDUE 27 31 CELL ATTACHMENT SITE (POTENTIAL).  
FT RESIDUE 31 31 CELL ATTACHMENT SITE (POTENTIAL).  
SQ SEQUENCE 155 AA: 27380 MW: 35236.64KDa(16060) CHS24;  
Query Match: 50.1%; Score 411.5; DB 1; Length 155;  
Match: 45; Conservative: 17; Miscellaneous: 5; Gaps: 2;  
QY 1 ALPHAFITTED--KFHPLKDFKFLKCNHRLALDFOVVOGHSRHOHQ 57  
DB 2 AMGLTTLTLEDESSAAPPFHFFKFKLCONGFGRHLNDDVDSESLK 61  
QY 58 IQLASGVETIKSTQTQALMCLDVLGVSQDSCELCPIHEHTPIETSKIA 117  
DB 61 LAGLRNEHVSVIGCVANLAKMEKLASVCNCTVFESNNVTYSKIS 121  
QY 118 EMNVYLKNGSKSGPTKTKTGQAIIPLFPYS 153  
DB 122 --SHVALRTQVLYBCTPGQALPLFGNS 155  
RESULT 9  
FPZ CHECK STANDARD; PROT: 158 AA.  
AC AC 14480; 1996 (Ref. 3), Contest  
DT 01-FEB-1996 (Ref. 3), Last sequence update  
DT 28-FEB-2003 (Ref. 4), Last annotation update  
DB Protein-binding growth factor 2 precursor (UBOF-2) (Basic fibroblast  
DB GRP OK F-2). (SP07)  
OS Gallus gallus (Chicken)  
OC Eukarya; Metazoa; Chordata; Vertebrata; Butelelalomoni;  
OC Gallus; Gallinae; Aves; Megathere; Galliformes; Phasianidae; Phasianinae;  
OK NCBI\_TaxID=9031;  
OK (1)  
OK MEDLINE: 93245597; PubMed: 1674466;  
OK MEDLINE: 93245597; PubMed: 1674466;  
OK Bojda A.Z., Selzer R., Meloyra C.:  
OK "Expression of alternatively spliced bFGF first coding exons and  
OK their role in embryogenesis.";  
OK Biol. 157:110-118(1995).  
XL -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS  
CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN  
CC CONCENTRATION RANGE 5-100 NG/ML. THESE GROWTH FACTORS  
CC -1- SUBUNIT: MONOMER.  
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES  
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.  
CC The SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC CC by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>).  
CC DR PMR: L26136; AAA15113.1.-.  
DR MSP: P00018; UNP0F:  
DR PRINTS: PR00242; ILIH0GF.  
DR PROBLEM: P000483; ID: UNP0F:  
DR PRINTS: PR00242; ILIH0GF.  
DR PROSITE: PS00247; HB0F; 1.  
GM Growth Factor; Mitogen; Angiogenesis; Hepatic-binding.  
FT PROPEP 1 12 BY SIMILARITY.  
FT SITE 30 34 HEPARIN-BINDING GROWTH FACTOR 2.  
FT BINDING 12 34 HEPARIN-BINDING GROWTH FACTOR 2.



[illegible][illegible]





[illegible]

	Query Match	39.6%; Score 327; DB 13;	Length 125;
	Best Local Similarity	52.8%; Fred. No. 1-1e-5;	
	Matches	57; Conservative 16; Mismatches 42; Indels 2; Gaps 1;	
DY	27 LYSNCHGKILIPVDTQTEBHQDGLQSASVPVTICTETQVLAMTDL 86		
DY	1 LLYCNKHFIINSDVFQVAARESDITLQLQERGVSTKVQVMANSLMDGR 69		
DY	87 LVGSCTNECLFELLENHNTOTYLISKWKNVPGKLNSCGPFGFTQAFLP 146		
DY	63 ILMATLVTFEPPFELENNNTCCSRKYSD--HYVALKTQVSNGTAQGALIF 118		
DY	147 LGUPVES 153		
DY	113 LGMANS 125		
RESULT 9			
ID	Q49P12	PRELIMINARY:	FRT: 62 AA.
DB	01-JUN-2002 (TrEMBLrel_21, Created)		
UT	01-JUN-2002 (TrEMBLrel_21, Last sequence update)		
UT	01-MAR-2003 (TrEMBLrel_23, Last annotation update)		
OS	Homo sapiens (Human)		
GO	PWP-1 cellular growth factor 1 (Fragment).		
DY	Eque caballus (Horse).		
OC	Bovidae; Cetartiodactyla; Chordata; Vertebrates; Euarchontomys;		
OC	Sukarya; Metazoa; Eumetazoa; Cephalochordata; Squamata; Agnatha;		
NCBI TaxID=9786;			
SEQUENCE FROM N.A.			
RP	Metzer B., Bollwein H., Klingenstein R.;		
RT	"Expression of horse endostromin.";		
RT	Submitted (MAR 2002) to the EMBL/GenBank/DDBJ databases.		
OK	Interfer: IPRO02348; ILI_HDPF.		
UK	Pfam: PF00467; PUF: 1.		
DK	Protein: p000081; ILI_HDPF: 1.		
PK	NOMTER 59		
FT	NOMTER 62 62		
SO	SEQUENCE 62 AA; 6851 MW; Q49P12ID79348O CIRC64;		
Query Match	39.1%; Score 324; DB 5;	Length 62;	
Best Local Similarity	52.8%; Fred. No. 1-1e-5;		
Matches	51; Conservative 16; Mismatches 35; Indels 0; Gaps 0;		
RESULT 10			
ID	Q49R1	PRELIMINARY:	FRT: 59 AA.
AC	Q49R1: 2005 (TrEMBLrel_13, Created)		
AD	01-MAY-2005 (TrEMBLrel_13, Last sequence update)		
UT	01-MAR-2003 (TrEMBLrel_23, Last annotation update)		
UT	Acidic fibroblast growth factor (Fragment).		
OS	Homo sapiens (Human)		
OC	Sukarya; Metazoa; Chordata; Vertebrates; Euarchontomys;		
OC	Mammalia; Eutheria; Primates; Carnivaria; Rodentia; Homo.		
NCBI TaxID=9606;			
SEQUENCE FROM N.A.			
RX	MEDLINE=93181239; PubMed=7680102;		
RT	Claudio A., Chen H., Choi M.M., Wang W.P., Harris S.E..		
RT	"Cloning of two novel forms of human acidic fibroblast growth factor (aDFP) cDNA.";		
RT	Nucleic Acids Res 21:489-495(1993).		
RU	Interfer: IPRO02348; ILI_HDPF.		
DR	MSFP: P55230; ZAKM.		
DK	Protein: p00081; ILI_HDPF: 1.		
PK	NOMTER 59 59		
FT	NOMTER 59 59		
SO	SEQUENCE 59 AA; 6404 MW; 95948764647AAO CIRC64;		
Query Match	37.9%; Score 313; DB 8;	Length 59;	
Best Local Similarity	100.0%; Fred. No. 1e-24;		
Matches	59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
RESULT 11			
ID	Q49S1	PRELIMINARY:	FRT: 59 AA.
DB	01-NOV-1996 (TrEMBLrel_01, Created)		
UT	01-NOV-1996 (TrEMBLrel_01, Last sequence update)		
UT	01-MAR-2003 (TrEMBLrel_23, Last annotation update)		
OS	Homo sapiens (Human)		
GO	Transplantation 56:1177-1178(1993).		
OC	Eukaryota; Metazoa; Chordata; Vertebrates; Euarchontomys;		
OC	Mammalia; Eutheria; Primates; Carnivaria; Rodentia; Homo.		
NCBI TaxID=9606;			
SEQUENCE FROM N.A.			
RX	MEDLINE=94069734; PubMed=7504343;		
RT	Zhao X.H., York T.K., Herbert M., Fries W.H., Miller O.G.;		
RT	"Isolation and characterization of complementary DNAs encoding growth factor-1 and cytokine genes in human cardiac allografts and T cells.";		
RU	Interfer: IPRO02348; ILI_HDPF.		
DR	MSFP: P55230; ZAKM.		

DR Pfam: PF00167; FGF, 1.  
DR ProDom: PD00093; IL1\_HBDF; 1.  
SO SEQUENCE 59 AA: 6555 MW: 3030364847140A CDS64;  
Query Match 36.4%; Score 302; DB 4; Length 59;  
Accession: J047326.1; Species: Mus musculus; Match: 59; Conservative: 14; Mismatches: 0; Indels: 0; Gaps: 0;  
QY 1 ABGGTTTATATKPNTPKPKKELVCSNGHFRIPDTOTVDTNSQDH 55  
DB 2 ABGGTTTATATKPNTPKPKKELVCSNGHFRIPDTOTVDTNSQDH 56  
RESULT 12  
Q04588  
ID Q04588 PRELIMINARY; FMT: 60 AA.  
AC Q04588; 1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE Acidic fibroblast growth factor (Fragment).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
NCBI\_TaxID: 9606;  
XP SEQUENCE FROM N.A.  
RA MEDLINE:4059734; PubMed:750134;  
EA Zhao X.M., Tech T.K., Hebert M., Friat W.N., Miller G.G.;  
RT The expression of acidic fibroblast growth factor (heparin-binding  
RT growth factor-1) and cytokine genes in human cardiac allografts and T  
RT cells.  
RL Transplantation 56:1177-1182(1993).  
RW SEQUENCE FROM N.A.  
RX MEDLINE:5202457; PubMed:1378643;  
RA Li Y.L., Xia H., Golden J.A., Michalsen A.A.J., Goetzl E.J.;  
RT "Lactoid": fibroblast growth factor protein generated by alternate  
RT splicing acts like an antagonistic.  
RL J. Exp. Med. 175:1073-1080(1992).  
DR EMBL: S6792; X02558.1; -.  
DR EMBL: S6792; X02558.1; -.  
DR HSP: P05335; 2AM.  
DR InterPro: IPR002346; IL1\_HBDF.  
DR Pfam: PF00167; FGF, 1.  
DR ProDom: PD00093; IL1\_HBDF; 1.  
FT NON\_TER 60  
SQ SEQUENCE 60 AA: 6597 MW: 3536840644734 CDS64;  
Query Match 36.4%; Score 302; DB 4; Length 60;  
Accession: J047326.1; Species: Mus musculus; Match: 59; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
QY 1 ABGGTTTATATKPNTPKPKKELVCSNGHFRIPDTOTVDTNSQDH 55  
DB 2 ABGGTTTATATKPNTPKPKKELVCSNGHFRIPDTOTVDTNSQDH 56  
RESULT 13  
Q04587  
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AC Q04587; 1996 (TrEMBLrel. 15, Created)  
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DE Basic fibroblast growth factor (Fragment).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
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RA MEDLINE:2522661; PubMed:1078967;  
EA Nguyen A., Blocher S., Gortz F., Fickel J.;  
RT Identification of growth factors in the nuclei of rat liver (Capreolus  
RT capreolus).  
RL Anal. Biochem. 261: 64-68(1998).  
DR EMBL: AF23287; AA7326.1; -.  
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DR Pfam: PF00167; FGF, 1.  
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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
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RA MEDLINE:2522661; PubMed:1078967;  
EA Nguyen A., Blocher S., Gortz F., Fickel J.;  
RT Identification of growth factors in the nuclei of rat liver (Capreolus  
RT capreolus).  
RL Anal. Biochem. 261: 64-68(1998).  
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RP MEDLINE:2522661; PubMed:1078967;  
RA Nguyen A., Blocher S., Gortz F., Fickel J.;  
RT "Alterations in Collagen and Elastin Gene Expression in Fetal  
RT Pulmonary Vessels in Monkeys Following Prenatal Nicotine Exposure: A  
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DR EMBL: AF23279; AA31962.1; -.  
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DT 01-JUN-1996 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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XP SEQUENCE FROM N.A.  
RA Zhang Y.-X., Hantawa K.V.;  
RT Identification of growth factors in the nuclei of rat liver (Capreolus  
RT capreolus).  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF01226; AA84020.1; -.  
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[illegible]









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[illegible]



[illegible]

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 : Patent No. 5691220  
 : INVENTOR: LUYUAN LI  
 : APPLICANT: Andrew P. Seldon  
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 : APPLICANT: LUYUAN LI  
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 : TITLE OF INVENTION: Surface Loop Structural Ana-  
 : logues of Polymer Logos of Fibroblast Growth Factors  
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 : NAME OF SPONSOR: N/A  
 : NAME OF SENDER: N/A  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: American Cyanamid Company  
 : ADDRESSEE: Patent Law Department  
 : STREET: One Cyanamid Plaza  
 : CITY: East Nyack  
 : STATE: NJ  
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 : COUNTRY: United States  
 : ZIP: 07470-4426  
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 : COMPUTER: IBM PC  
 : MEDIA: 3.5 inch diskette  
 : COMPUTER: IBM PC  
 : OPERATING SYSTEM: MS DOS  
 : SOFTWARE: Word Processor

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2  FILING DATE: August 13, 1994
3  PRIORITY NUMBER:
4  APPLICATION NUMBER: 08/126,973
5  FILING DATE: September 24, 1993
6  ATTORNEY/AGENT INFORMATION:
7  NAME: Miradach Barnhart
8  REFERENCE/DOCKET NUMBER: 854-00688
9  REFERENCE/DOCKET NUMBER: 854-006CIP [32,063]
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: 201-631-3242
12 TELEX: 201-911-3105
13 FAX: 201-911-3105
14 ADDRESS: 16
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 477 bases
17 TYPE: nucleic acid
18 STRANDEDNESS: single
19 ORIENTATION: 5' to 3'
20 MOLECULE TYPE:
21 DESCRIPTION: DNA encoding a protein
22 FRAGMENT TYPE: entire sequence
23 SOURCE: constructed
24 FEATURE:
25 OTHER INFORMATION: FGF-2 having surface loop
26 OTHER INFORMATION: residues 116 to 122 replaced with corresponding

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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
```

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13: /cgn2_6/ptodata/1/pubpna/US09_NSW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCONB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCONB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCONB.seq.*

```

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17: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq*
18: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq*
19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	Score	Match Length	DB ID	Description
1	825 100 0 468 9 115-08-926-916-3				Sequence 1 Apple

2	825	100.0	468	9	US-09-929-945-3	Sequence 3, Appli
3	825	100.0	468	15	US-10-280-864-3	Sequence 3, Appli
4	825	100.0	468	17	US-10-549-480-3	Sequence 3, Appli

5	825	100.0	490	15	US-10-388-410-8	Sequence 8, Appli
6	825	100.0	490	17	US-10-641-643-1390	Sequence 1390, Ap
7	825	100.0	630	9	US-09-929-918-1	Sequence 1, Appli
8	825	100.0	630	9	US-09-929-945-1	Sequence 1, Appli

9	825	100.0	630	15	US-10-280-864-1	Sequence 1, Appli
10	825	100.0	630	17	US-10-649-480-1	Sequence 1, Appli
11	825	100.0	618	10	US-09-902-460-3	Sequence 3, Appli

12	825	100.0	990	9	US-09-939-918-10	Sequence 10, Appl
13	825	100.0	4087	14	US-10-044-090-235	Sequence 225, App
14	759.5	92.1	630	9	US-09-939-918-6	Sequence 6, Appl
15	759.5	92.1	630	9	US-09-939-945-6	Sequence 6, Appl

16	759.5	92.1	630	15	US-10-280-864-6	Sequence 6, Appli
17	759.5	92.1	630	17	US-10-649-480-6	Sequence 6, Appli
18	721	87.4	630	9	US-09-939-918-4	Sequence 4, Appli

19	721	87.4	630	9	US-0939-945-4	Sequence 4, Appli
20	721	87.4	630	15	US-10-280-864-4	Sequence 4, Appli
21	721	87.4	630	17	US-10-649-480-4	Sequence 4, Appli
22	435.5	50.4	468	13	US-10-389-821-5	Sequence 5, Appli

23	413.5	50.1	468	9	US-09-802-365-5	Sequence 5, Appli
24	413.5	50.1	468	9	US-09-806-856-5	Sequence 5, Appli
25	411.5	49.9	1374	10	US-09-075-964-26	Sequence 26, Appli

26	404.5	49.0	465	9	US-09-749-7283-8	Sequence 8, Appl
27	404.5	49.0	465	10	US-09-861-237-25	Sequence 25, Appl
28	404.5	49.0	465	15	US-10-189-360-52	Sequence 52, Appl
29	404.5	49.0	474	9	US-09-802-365-7	Sequence 7, Appl

30	404.5	49.0	474	9	US-09-886-856-7	Sequence 7, Appl
31	404.5	49.0	483	9	US-09-826-210-1	Sequence 1, Appl
32	404.5	49.0	489	9	US-09-934-706-11	Sequence 11, Appl

33	404.5	49.0	489	13	US-10-344-634-7	Sequence 7, Appli
34	404.5	49.0	489	15	US-10-395-541-4	Sequence 4, Appli
35	404.5	49.0	630	16	US-10-408-415-4	Sequence 4, Appli
36	404.5	49.0	1182	13	US-10-344-634-13	Sequence 13, Appli

Sequence 53, Appl	Sequence 24, Appl	Sequence 80, Appl
37 404.5 49.0 1230 15 US-10-189-360-53	38 404.5 49.0 1231 10 US-09-861-237-24	39 404.5 49.0 1231 15 US-10-189-360-80

41	404.5	49.0	1251	15	US-10-189-360-74	Sequence 74, Appl
40	404.5	49.0	1251	10	US-09-861-257-75	Sequence 75, Appl
40	404.5	49.0	1251	10	US-09-861-257-77	Sequence 77, Appl
41	404.5	49.0	1251	15	US-10-189-360-74	Sequence 74, Appl
42	404.5	49.0	1260	10	US-09-861-257-75	Sequence 75, Appl
43	404.5	49.0	1260	15	US-10-189-360-72	Sequence 72, Appl

44	404.5	49.0	1266	10	US-09-661-257-78	Sequence 78, Appl
45	404.5	49.0	1266	15	US-10-189-360-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1

US-09-923-918-3  
; Sequence 3, Application US/09929918  
; Patent No. US2002009678A1

GENERAL INFORMATION:  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.

APPLICANT: Vozianov, Olexsandr  
TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF  
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES

THE REFERENCE: FRAUD, USA



[illegible][illegible][illegible]

[illegible]





**Source**

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